SEARCH 101 Case # 08/327,522

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(FILE 'USPAT' ENTERED AT 14:45:31 ON 31 JUL 95)
L1 14861 S OLIGO# OR OLIGONUCLEOTIDE# OR DNA OR RNA OR POLYNUCLEOTI
DE#
L2 207828 S ARRAY# OR CHIP# OR BIOCHIP#
L3 301 S L1 (P) L2
L4 90 S L1 (5A) L2
L5 265637 S SEQUENC?
L6 6458 S L1 (P) L5
L7 150 S L2 (P) L6
L8 78 S L7 NOT L4
=> d L4 1-90 cit kwic

1. 5,436,136, Jul. 25, 1995, Repressible yeast promoters; Albert Hinnen, et al., 435/69.1, 172.3, 254.2, 320.1; 536/24.1; 935/28, 37 [IMAGE AVAILABLE]

US PAT NO: 5,436,136 [IMAGE AVAILABLE] L4: 1 of 90

SUMMARY:

BSUM(50)

The . . . in a tandem array or at different locations of the hybrid vector. Preferred hybrid vectors contain one DNA insert or **DNA** inserts in a tandem **array**.

2. 5,436,130, Jul. 25, 1995, Multiple tag labeling method for DNA sequencing; Richard A. Mathies, et al., 435/6, 91.5; 436/94, 164, 172, 173; 935/77 [IMAGE AVAILABLE]

US PAT NO: 5,436,130 [IMAGE AVAILABLE] L4: 2 of 90

DETDESC:

DETD(2)

A suitable, two-color capillary **array** electrophoresis scanner for detecting **DNA** sequencing is shown in FIG. 1. It consists of two confocal detection channels that are coupled into the optical system. . .

3. 5,434,340, Jul. 18, 1995, Transgenic mice depleted in mature T-cells and methods for making transgenic mice; Paulus J. A. Krimpenfort, et al., 800/2; 435/172.3; 800/DIG.1; 935/111 [IMAGE AVAILABLE]

US PAT NO: 5,434,340 [IMAGE AVAILABLE] L4: 3 of 90

DETDESC:

DETD(29)

As shown schematically in FIG. 2, the encoding segments for the TCR genes are scattered over large **arrays** of chromosomal **DNA**. Like the immunoglobulin genes, specific V, D and J segments are fused together to generate a complete V coding region. . .

4. 5,434,049, Jul. 18, 1995, Separation of polynucleotides using

supports having a plurality of electrode-containing cells; Kazunori Okano, et al., 435/6; 422/68.1, 101; 436/72, 94, 807, 809; 536/25.4 [IMAGE AVAILABLE]

US PAT NO: 5,434,049 [IMAGE AVAILABLE] L4: 4 of 90

ABSTRACT:
A . . . of target polynucleotides in a sample on a single reaction chip and a method for separating a plurality of target **polynucleotides** are provided. On the reaction **chip** are arranged a plurality of independent cells for capturing different target polynucleotides. Different probes are immobilized onto the individual cells,. . .

SUMMARY:

BSUM(8)

It is an objective of the present invention to provide a **polynucleotide** capturing **chip** capable of simultaneously capturing a plurality of target polynucleotides, and also to provide a method for detecting a plurality of. . .

SUMMARY:

BSUM(9)

In the **polynucleotide** capturing **chip** with immobilized probes complementary to target polynucleotides in accordance with the present invention, individually different probes for a plurality of. . .

SUMMARY:

BSUM(10)

In . . . target polynucleotides and a process of bonding a labeling substance, a plurality of target polynucleotides are measured using the aforementioned **polynucleotide** capturing **chip** as the **polynucleotide** capturing support.

SUMMARY:

BSUM(11)

According . . . capturing support with immobilized probes complementary for the target polynucleotides and then separating the target polynucleotides, each cell of the **polynucleotide** capturing **chip** to be used as the **polynucleotide** capturing support also functions as an electrode for eluting the target polynucleotides, wherein the electric fields applied to such electrodes. . .

SUMMARY:

BSUM(12)

The . . . conditions after the addition of a sample solution, the target polynucleotides contained in the sample are captured onto the reaction **chip**. Then, the individual target **polynucleotides** are captured onto different cells with the immobilized individual polynucleotide probes in accordance with the present invention. For the simultaneous. . .

SUMMARY:

BSUM(13)

For . . . be contaminated with each other. Secondly, the present invention is characterized in the method for eluting target polynucleotides. The target **polynucleotides** captured onto the **chip** via hybridization reaction are readily eluted via heating and the like. The present invention is constituted, as is shown in. . .

SUMMARY:

BSUM(14)

When . . . hybrid between the two types of the polynucleotides, namely the target polynucleotide and the probe, is formed. Only if the **polynucleotide** probe is immobilized onto a **chip**, the target **polynucleotide** should be captured onto the **chip**. In accordance with the present invention, it is required to arrange a plurality of cells on a chip. Therefore, such. . .

DETDESC:

DETD(11)

In . . . explanation will follow regarding a method for preparing a reaction chip having a plurality of independent cells with immobilized different **polynucleotide** probes within the single reaction **chip**; and a method for detecting target polynucleotides using the same.

DETDESC:

DETD(19)

As has been described above, the present invention is used for detecting a plurality of target **polynucleotides** on a single reaction **chip**. Thus, the present invention proposes an advantage in that only a single reaction procedure is needed for carrying out a. . .

DETDESC:

DETD(48)

As has been described above, also, the present invention enables the simultaneous detection of a plurality of target **polynucleotides** with a single reaction **chip**, so it is advantageous to require less reaction procedures compared with the conventional method requiring to prepare one reaction **chip** per target **polynucleotide**. Also, the volume of a sample solution should be less because the solution is used for only a single reaction. . .

5. 5,432,081, Jul. 11, 1995, Host cells transformed with the E. coli glucoronide permease gene; Richard A. Jefferson, 435/252.3, 183, 240.2, 252.33, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,432,081 [IMAGE AVAILABLE] L4: 5 of 90

DETDESC:

DETD(163)

Plasmid . . . Biol. 5:3484-3496. The strain used was DH408, lacking glucuronidase activity (Horch et al., 1984, Science 223:496-498). Lines carrying the injected **DNA** as high-copy extrachromosomal tandem **arrays** were obtained from the F2 generation of the injected worms. Stability and physical properties of the tandem arrays were similar. .

6. 5,429,807, Jul. 4, 1995, Method and apparatus for creating biopolymer arrays on a solid support surface; Robert S. Matson, et al., 422/131, 101, 102, 116; 435/6, 287; 436/518; 935/88 [IMAGE AVAILABLE]

US PAT NO: 5,429,807 [IMAGE AVAILABLE] L4: 6 of 90

SUMMARY:

BSUM(6)

DNA . . . WO 89/10977, it disclosed that DNA can be synthesized onto a glass slide to form a structured one-dimensional matrix or **array** of **polynucleotides**. The synthesized material is left attached to the glass slide which is then applied in a hybridization reaction process for. . .

DETDESC:

DETD(14)

Referring to FIG. 7, the end result is a parallel one-dimensional (M.times.1) matrix or **array** 74 of **polynucleotide** strands formed on the derivatized surface 58 of the sheet 56, each element 76 of the array being in the. . .

DETDESC:

DETD(17)

At . . . cells. To illustrate this point, let the bands 76a, 76b in array 74 and bands 84a and 84b in the **array** 82 contain **polynucleotides** which have the following sequences (the left most nucleotide is attached to the sheet 56):

CLAIMS:

CLMS(20)

20. . . .
the applicator with respect to the activated surface and applying reagents to said activated surface to synthesize a first one-dimensional **array** of **polynucleotides**;
repositioning the applicator and applying reagents to said activated surface to synthesize a second one-dimensional **array** of **polynucleotides** in a manner where said second one-dimensional array overlaps the first one-dimensional array to form a two-dimensional array of cells. . .

7. 5,428,007, Jun. 27, 1995, Genetically engineered low oxygen affinity mutants of human hemoglobin; James J. Fischer, et al., 514/6; 435/7.23, 69.1, 69.6, 172.3, 240.2, 252.3, 320.1; 514/2, 12; 530/350, 385; 536/22.1, 23.1, 23.5 [IMAGE AVAILABLE]

US PAT NO: 5,428,007 [IMAGE AVAILABLE] L4: 7 of 90

SUMMARY:

BSUM(28)

DNA sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

8. 5,427,780, Jun. 27, 1995, Composition comprising Mullerian inhibiting substance-like polypeptides; Richard L. Cate, et al., 424/85.1; 514/12; 530/351, 399 [IMAGE AVAILABLE]

US PAT NO: 5,427,780 [IMAGE AVAILABLE] L4: 8 of 90

DETDESC:

DETD(4)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

9. 5,427,663, Jun. 27, 1995, Microlithographic array for macromolecule and cell fractionation; Robert H. Austin, et al., 204/180.1, 299R; 209/127.1, 155, 156 [IMAGE AVAILABLE]

US PAT NO: 5,427,663 [IMAGE AVAILABLE] L4: 9 of 90

DRAWING DESC:

DRWD(9)

FIG. 6 is a plan view of the sorting apparatus shown in FIG. 1 with the obstacles enlarged to illustrate **DNA** molecules migrating through the **array**;

DETDESC:

DETD(43)

In . . . are illustrated as long arrows. The direction of the arrows indicates the direction of migration of DNA molecules 68. As **DNA** molecules migrate through **array** 38 of obstacles 39, large bodies of DNA molecules may become hooked by obstacles 39 and may become trapped. The. . .

DETDESC:

DETD(45)

The . . . imaging of long megabase DNA fragments. The staggered configuration, having a higher possibility of hooking the DNA molecules as the **DNA** molecules migrate through the **array**, can be used to more directly test the role of DNA relaxation and hooking in the mobility of DNA molecules.

10. 5,424,186, Jun. 13, 1995, Very large scale immobilized polymer synthesis; Stephen P. A. Fodor, et al., 435/6; 436/518, 527, 528, 809; 536/25.3, 25.31, 25.32 [IMAGE AVAILABLE]

US PAT NO: 5,424,186 [IMAGE AVAILABLE] L4: 10 of 90

ABSTRACT:
A . . . a first nucleotide to couple the nucleotide to the substrate in the first predefined region. By repeating these steps, an **array** of diverse **oligonucleotides** is formed on the substrate.

CLAIMS:

CLMS(8)

8. . . .
a part of said second area; and
e) performing additional irradiating and nucleotide contacting and coupling steps so that a matrix **array** of at least 100 different **oligonucleotides** is formed on said surface, each different oligonucleotide synthesized in an area of less than 0.1 cm.sup.2, whereby said different. . .

11. 5,420,328, May 30, 1995, Methods for the synthesis of phosphonate esters; David A. Campbell, 558/110 [IMAGE AVAILABLE]

US PAT NO: 5,420,328 [IMAGE AVAILABLE] L4: 11 of 90

SUMMARY:

BSUM(29)

The invention further provides a method of forming an array of phosphonate esters or phosphonic acids. These defined **arrays** or libraries of **oligonucleotide** will find a variety of uses, for example, to screen the substrate-bound compounds for biological activity.

12. 5,416,008, May 16, 1995, Cross-regulation of gene expression in recombinant cells; James E. Bailey, et al., 435/69.1, 71.1, 71.2, 172.3, 252.33, 254.21 [IMAGE AVAILABLE]

US PAT NO: 5,416,008 [IMAGE AVAILABLE] L4: 12 of 90

DETDESC:

DETD(4)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentose moieties.

13. 5,412,087, May 2, 1995, Spatially-addressable immobilization of oligonucleotides and other biological polymers on surfaces; Glenn H. McGall, et al., 536/24.3; 435/181; 436/532; 530/816; 536/22.1 [IMAGE AVAILABLE]

US PAT NO: 5,412,087 [IMAGE AVAILABLE] L4: 13 of 90

SUMMARY:

BSUM(16)

Thus, . . . of oligonucleotides on a glass surface derivatized with a caged thiol reagent. The method can be used to fabricate large **arrays** of **oligonucleotide** probes.

DETDESC:

DETD(34)

In . . . can be repeated on a different region of the surface with a different anti-ligand. In this fashion, a small, dense **array** of, e.g., **oligonucleotide** probes, can be prepared.

DETDESC:

DETD(82)

Specific Hybridization of Nucleic Acids to Immobilized

14. 5,403,708, Apr. 4, 1995, Methods and compositions for determining the sequence of nucleic acids; Thomas M. Brennan, et al., 435/6, 91.52; 436/94; 536/24.33, 25.32 [IMAGE AVAILABLE]

US PAT NO: 5,403,708 [IMAGE AVAILABLE] L4: 14 of 90

SUMMARY:

BSUM(4)

The . . . al. (1989) FEBS Letters 256:118; Bains, et al. (1988) J. Theoro. Biol. 135:303; and Drmanac, et al. (1988) Genomics 4:114), **array** determination of **DNA** sequence by mass spectrometry (U.S. Pat. No. 5,003,059), as well as suggestions to use isotopic sulfur (Brennan, et al., Biological. . .

15. 5,401,642, Mar. 28, 1995, Vectors and methods for making such vectors and for expressing cloned genes; Walter C. Fiers, et al., 435/69.1, 69.5, 69.51, 69.52, 69.6, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,401,642 [IMAGE AVAILABLE] L4: 15 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

16. 5,397,703, Mar. 14, 1995, Method for generation of antibodies to cell surface molecules; Mark De Boer, et al., 435/172.2, 172.3; 530/389.1 [IMAGE AVAILABLE]

US PAT NO: 5,397,703 [IMAGE AVAILABLE] L4: 16 of 90

DETDESC:

DETD(11)

The . . . of large coding sequences, the oligonucleotide coding sequence can be synthesized through a series of cloning steps involving a tandem **array** of multiple **oligonucleotide** fragments corresponding to the coding sequence (Crea; Yoshio et al.; Eaton et al.). Oligonucleotide coding sequences can be amplified and. . .

17. RE 34,851, Feb. 7, 1995, Biosynthesis of 2 keto-L-gulonic acid; Ronald F. Manning, et al., 435/252.32, 136, 137, 138, 172.3, 252.3, 320.1; 536/23.1, 23.2, 24.1; 935/29, 56, 72 [IMAGE AVAILABLE]

US PAT NO: RE 34,851 [IMAGE AVAILABLE] L4: 17 of 90

DETDESC:

DETD(3)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

18. 5,384,261, Jan. 24, 1995, Very large scale immobilized polymer

synthesis using mechanically directed flow paths; James L. Winkler, et al., 436/518; 422/134, 149; 435/7.1, 968, 969, 970, 973; 436/501, 527, 531, 532, 807, 809; 530/334, 335, 337 [IMAGE AVAILABLE]

US PAT NO: 5,384,261 [IMAGE AVAILABLE] L4: 18 of 90

SUMMARY:

BSUM(5)

Accordingly, improved methods of forming large **arrays** of peptides, **oligonucleotides**, and other polymer sequences in a short period of time have been devised. Of particular note, Pirrung et. al., PCT. . .

19. 5,376,526, Dec. 27, 1994, Genomic mismatch scanning; Patrick Brown, et al., 435/6, 91.1; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,376,526 [IMAGE AVAILABLE] L4: 19 of 90

SUMMARY:

BSUM(43)

The DNA that is probed may take a variety of forms, but essentially consists of a physically-ordered **array** of **DNA** sequences that can be related back to the physical arrangement of the corresponding sequences in the genome (See Boyle, et. . .

SUMMARY:

BSUM(49)

An . . . and reannealed. The selected mismatched hybrid sequences are then labeled and used as probes for hybridization to a physically ordered **array** of a genomic **DNA** sample. Because regions of the genome that lack heterozygosity are unable to produce single-copy DNA hybrids with base mismatches, these. . .

SUMMARY:

BSUM(52)

For . . . blunt end ligation or other composition for labeling the sequences to provide probes. Other components such as a physically ordered **array** of immobilized **DNA** genomic clones or metaphase chromosomes, automated systems for determining and interpreting the hybridization results, software for analyzing the data, or. . .

20. 5,368,823, Nov. 29, 1994, Automated synthesis of oligonucleotides; Royal A. McGraw, et al., 422/134, 111, 116; 435/287, 289; 935/88 [IMAGE AVAILABLE]

US PAT NO: 5,368,823 [IMAGE AVAILABLE] L4: 20 of 90

DETDESC:

DETD(44)

The . . . the device are to be coupled. Oligo ID #096A will be synthesized in the first column of the linear column **array** and **oligo** ID #095B will be synthesized in the 32nd and last column of the array. As previously mentioned, the prototype device. . .

21. 5,366,878, Nov. 22, 1994, Method of site-specific alteration of RNA

and production of encoded polypeptides; Thoru Pederson, et al., 435/91.3, 91.1; 514/44; 536/23.1, 24.5, 25.1, 25.3; 935/2, 34, 36 [IMAGE AVAILABLE]

US PAT NO: 5,366,878 [IMAGE AVAILABLE] L4: 21 of 90

SUMMARY:

BSUM(5)

Typically, . . . level, by recombinant DNA techniques which rely on the use of restriction endonucleases. However, restriction endonucleases available have a limited **array** of target sites in **DNA** (usually palindromic hexanucleotide or octanucleotide sequences). Deletion of a particular in-frame trinucleotide or trinucleotides may not be possible because there. . .

22. 5,365,455, Nov. 15, 1994, Method and apparatus for automatic nucleic acid sequence determination; Clark Tibbetts, et al., 364/497, 413.01, 413.07, 554; 395/924 [IMAGE AVAILABLE]

US PAT NO: 5,365,455 [IMAGE AVAILABLE] L4: 22 of 90

SUMMARY:

BSUM(3)

Current methods of DNA sequencing rely upon electrophoretic separation of incremental **oligonucleotides**. These stochastic **arrays** of oligomers are produced usually by one of two methods. The Maxam-Gilbert method (Proc. Natl. Acad. Sci. USA, 74: 560-564. . .

23. 5,354,855, Oct. 11, 1994, RNA Ribozyme which cleaves substrate RNA without formation of a convalent bond; Thomas R. Cech, et al., 536/24.1, 23.1 [IMAGE AVAILABLE]

US PAT NO: 5,354,855 [IMAGE AVAILABLE] L4: 23 of 90

DETDESC:

DETD(33)

Earlier . . . therein by insertions and deletions to obtain other self-splicing IVS RNA's. In like manner, we could alter the L-19 IVS **RNA** to obtain an **array** of **RNA** sequence-specific endoribonuclease molecules. Thus three regions were found by Price et al. to be necessary for IVS self-splicing. Similar experiments. . .

24. 5,316,922, May 31, 1994, Method for indentifying and expressing proteins that recognize and adhere to specific probes; Stanley Brown, et al., 435/69.7, 7.32, 7.37, 7.8; 935/79 [IMAGE AVAILABLE]

US PAT NO: 5,316,922 [IMAGE AVAILABLE] L4: 24 of 90

DETDESC:

DETD(21)

To ensure that the inserts comprise random **arrays** of different semi-random **polynucleotides**, one can optionally sequence the nucleotides comprising the inserts. This step is optional.

25. 5,306,619, Apr. 26, 1994, Screening assay for the detection of DNA-binding molecules; Cynthia A. Edwards, et al., 435/6, 7.21, 7.23, 172.1, 172.3, 235.1; 436/501; 536/23.1, 23.4, 23.5, 23.6, 23.7 [IMAGE

AVAILABLE]

US PAT NO: 5,306,619 [IMAGE AVAILABLE] L4: 25 of 90

DETDESC:

DETD(104)

In practice, the size of sequences tested can be explored empirically for different sized test **DNA**-binding molecules. A wide **array** of sequences with increasing sequence complexity can be routinely investigated. This may be accomplished efficiently by synthesizing degenerate oligonucleotides and. . .

26. 5,298,489, Mar. 29, 1994, DNA sequences recombinant DNA molecules and processes for producing lipocortins III, IV, V and VI; Barbara P. Wallner, et al., 514/12; 435/69.1, 320.1; 530/350; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,298,489 [IMAGE AVAILABLE] L4: 26 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

27. 5,274,240, Dec. 28, 1993, Capillary array confocal fluorescence scanner and method; Richard A. Mathies, et al., 250/458.1; 204/180.1, 299R; 250/459.1, 461.1 [IMAGE AVAILABLE]

US PAT NO: 5,274,240 [IMAGE AVAILABLE] L4: 27 of 90

DRAWING DESC:

DRWD(7)

FIG. 5 is an image obtained by scanning a four-capillary **array** during a **DNA** separation;

28. 5,274,087, Dec. 28, 1993, cDNA coding for carcinoembryonic antigen (CEA); Thomas R. Barnett, et al., 536/23.5; 435/6, 172.3, 320.1; 536/24.3, 24.31; 935/11, 27 [IMAGE AVAILABLE]

US PAT NO: 5,274,087 [IMAGE AVAILABLE] L4: 28 of 90

SUMMARY:

BSUM(34)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

29. 5,270,201, Dec. 14, 1993, Artificial chromosome vector; Eric J. Richards, et al., 435/240.4, 240.1, 252.33, 254.2, 320.1; 536/23.1 [IMAGE AVAILABLE]

US PAT NO: 5,270,201 [IMAGE AVAILABLE] L4: 29 of 90

DETDESC:

DETD(155)

Highly . . . (1987)), features common to most higher eukaryotic organisms. The inventors then decided that the chromosomal location of the telomere-similar repetitive **DNA** **array** contained in the pAtT12 insert should be determined.

30. 5,268,463, Dec. 7, 1993, Plant promoter .alpha.-glucuronidase gene construct; Richard A. Jefferson, 536/23.7; 435/172.3, 200, 240.4, 320.1; 536/24.1 [IMAGE AVAILABLE]

US PAT NO: 5,268,463 [IMAGE AVAILABLE] L4: 30 of 90

DETDESC:

DETD(163)

Plasmid . . . Biol. 5:3484-3496. The strain used was DH408, lacking glucuronidase activity (Horch et al., 1984, Science 223:496-498). Lines carrying the injected **DNA** as high-copy extrachromosomal tandem **arrays** were obtained from the F2 generation of the injected worms. Stability and physical properties of the tandem arrays were similar. . .

31. 5,264,418, Nov. 23, 1993, Hemolymphopoietic growth factors, process for purifying and producing hemolymphopoietic growth factors and pharmaceutical compositions made therefrom; Peter J. Quesenberry, et al., 514/12; 435/172.3, 240.2; 514/2, 21; 530/399, 412, 413, 838 [IMAGE AVAILABLE]

US PAT NO: 5,264,418 [IMAGE AVAILABLE] L4: 31 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

32. 5,258,289, Nov. 2, 1993, Method for the selecting of genes encoding catalytic antibodies; Claude G. Davis, et al., 435/69.6; 424/805, 810; 435/69.7, 172.3, 188.5; 536/23.53 [IMAGE AVAILABLE]

US PAT NO: 5,258,289 [IMAGE AVAILABLE] L4: 32 of 90

DETDESC:

DETD(22)

To . . . ILQSSCDGGGHFPPTIQLL. The nucleic acid sequence encoding this peptide is constructed in a series of cloning steps, by generating a tandem **array** of multiple **oligonucleotide** fragments corresponding to the coding sequence of the complete target region generated. The final product is cut out of the. . .

DETDESC:

DETD(131)

The . . . for cloning in-frame into the polylinker region of pUC19 (Bethesda Research Laboratories). In a series of cloning steps, a tandem **array** of multiple **oligonucleotide** fragments corresponding to the coding sequence of the complete target region is generated. This overall

cloning strategy to generate synthetic. . .

33. 5,252,487, Oct. 12, 1993, Method and apparatus for determining the amount of oncogene protein product in a cell sample; James W. Bacus, et al., 436/63; 356/39; 382/129; 422/68.1, 82.09; 436/86, 164, 174, 813 [IMAGE AVAILABLE]

US PAT NO: 5,252,487 [IMAGE AVAILABLE] L4: 33 of 90

DETDESC:

DETD(2)

Referring . . . 26 to receive the enhanced DNA image signal and the enhanced oncogene protein product image signal and to store a **DNA** pixel **array** and an oncogene protein product pixel array therein. The image processor 28 is connected to a computer 32, in the present embodiment, an IBM personal computer model AT for processing of the **DNA** and oncogene protein product pixel **arrays**.

34. 5,242,811, Sep. 7, 1993, Production of human somatomedin C; Gary N. Buell, et al., 435/69.7, 69.1, 69.4, 172.3, 252.3, 252.33, 320.1; 536/23.1, 23.4, 23.51; 935/38 [IMAGE AVAILABLE]

US PAT NO: 5,242,811 [IMAGE AVAILABLE] L4: 34 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

35. 5,238,919, Aug. 24, 1993, Peptides that inhibit von Willebrand Factor binding to the platelet SPIB receptor; Theodore S. Zimmerman, et al., 514/8, 12, 13, 14, 822; 530/324, 325, 326, 383, 395 [IMAGE AVAILABLE]

US PAT NO: 5,238,919 [IMAGE AVAILABLE] L4: 35 of 90

DETDESC:

DETD(4)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses. Heterologous. . .

36. 5,231,009, Jul. 27, 1993, CDNAS coding for members of the carcinoembryonic antigen family; Thomas R. Barnett, et al., 435/240.2, 252.3; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,231,009 [IMAGE AVAILABLE] L4: 36 of 90

SUMMARY:

BSUM(35)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

37. 5,220,007, Jun. 15, 1993, Method of site-specific alteration of RNA and production of encoded polypeptides; Thoru Pederson, et al., 536/23.1, 22.1, 23.5, 25.1; 935/2, 8, 36 [IMAGE AVAILABLE]

US PAT NO: 5,220,007 [IMAGE AVAILABLE] L4: 37 of 90

SUMMARY:

BSUM(3)

Typically, . . . level, by recombinant DNA techniques which rely on the use of restriction endonucleases. However, restriction endonucleases available have a limited **array** of target sites in **DNA** (usually palindromic hexanucleotide or octanucleotide sequences). Deletion of a particular in-frame trinucleotide or trinucleotides may not be possible because there. . .

38. 5,219,727, Jun. 15, 1993, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/6, 91.2, 91.21; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,219,727 [IMAGE AVAILABLE] L4: 38 of 90

DETDESC:

DETD(25)

In . . . a third primer array is inserted into the internal standard plasmid between the 5' primer array and the 3' primer **array**. The third **oligonucleotide** **array** is comprised of a series of synthetic sequences wherein there is one sequence corresponding to each RNA for which the. . . RNA to be quantitated, the amplified product will contain within it a sequence identical to a portion of the third **oligonucleotide** **array**. Thus, both the amplified target and amplified standard DNA segments contain an identical internal segment providing a probe hybridization site,. . .

DETDESC:

DETD(26)

Where a third **oligonucleotide** **array** is included in the standard plasmid, the PCR reaction can be carried out without the use of label. It is. . .

39. 5,216,141, Jun. 1, 1993, Oligonucleotide analogs containing sulfur linkages; Steven A. Benner, 536/27.13, 27.2, 27.21, 28.4, 28.5, 28.53; 544/242, 264, 265, 267, 276 [IMAGE AVAILABLE]

US PAT NO: 5,216,141 [IMAGE AVAILABLE] L4: 39 of 90

SUMMARY:

BSUM(6)

The "complementarity rules" mentioned above could, in principle, guide the design of a molecule that presents to a natural **oligonucleotide** an **array** of hydrogen bond donor and acceptor groups that would form the basis for a specific binding to this oligonucleotide. However,. . .

DETDESC:

DETD(5)

An **oligonucleotide** analog presenting a specific **array** of hydrogen bond donor and acceptor groups will bind to any natural oligonucleotide that contains a sequence with a complementary. . .

40. 5,196,333, Mar. 23, 1993, DNA sequences involved in neuronal degeneration, multicellular organisms containing same and uses thereof; Marin Chalfie, et al., 435/240.1, 29, 69.1, 70.3; 536/23.5; 935/1, 19, 38 [IMAGE AVAILABLE]

US PAT NO: 5,196,333 [IMAGE AVAILABLE] L4: 40 of 90

DETDESC:

DETD(83)

The . . . if the DNA is not attached or otherwise integrated into the host's chromosomal DNA. Especially, those transformants which possess extrachromosomal **arrays** of the injected **DNA** may be genetically unstable. However, in one strain (uInl) the mutant phenotypes are stably inherited, and karyotype and Southern blot. . .

41. 5,175,384, Dec. 29, 1992, Transgenic mice depleted in mature T-cells and methods for making transgenic mice; Paulus J. A. Krimpenfort, et al., 800/2; 435/172.3; 800/DIG.1; 935/111 [IMAGE AVAILABLE]

US PAT NO: 5,175,384 [IMAGE AVAILABLE] L4: 41 of 90

DETDESC:

DETD(29)

As shown schematically in FIG. 2, the encoding segments for the TCR genes are scattered over large **arrays** of chromosomal **DNA**. Like the immunoglobulin genes, specific V, D and J segments are fused together to generate a complete V coding region. . .

42. 5,173,426, Dec. 22, 1992, DNAs encoding genetically engineered low oxygen affinity mutants of human hemoglobin; James J. Fischer, et al., 435/252.3, 69.6, 172.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,173,426 [IMAGE AVAILABLE] L4: 42 of 90

SUMMARY:

BSUM(28)

DNA sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

43. 5,169,941, Dec. 8, 1992, DNA sequences coding for the DR .beta.-chain locus of the human lymphocyte antigen complex and polypeptides, diagnostic typing processes and products related thereto; Bernard F. Mach, et al., 536/26.1; 435/69.3, 91.1, 91.41, 172.3, 240.2, 240.4, 252.31, 252.33, 252.34, 254.11, 254.2 [IMAGE AVAILABLE]

US PAT NO: 5,169,941 [IMAGE AVAILABLE] L4: 43 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent

pentoses.

44. 5,168,499, Dec. 1, 1992, Fault detection and bypass in a sequence information signal processor; John C. Peterson, et al., 371/11.3, 22.3 [IMAGE AVAILABLE]

US PAT NO: 5,168,499 [IMAGE AVAILABLE] L4: 44 of 90

SUMMARY:

BSUM(46)

The . . . processor that can locate highly similar segments or contiguous subsequences from any two data character streams (sequences) such as different **DNA** or protein sequences. The **chip** is implemented in a preferred embodiment using CMOS VLSI technology to provide the equivalent of about 400,000 transistors or 100,000. . .

45. 5,149,797, Sep. 22, 1992, Method of site-specific alteration of RNA and production of encoded polypeptides; Thoru Pederson, et al., 536/23.1; 435/183; 536/25.1; 935/8, 22 [IMAGE AVAILABLE]

US PAT NO: 5,149,797 [IMAGE AVAILABLE] L4: 45 of 90

SUMMARY:

BSUM(5)

Typically, . . . level, by recombinant DNA techniques which rely on the use of restriction endonucleases. However, restriction endonucleases available have a limited **array** of target sites in **DNA** (usually palindromic hexanucleotide or octanucleotide sequences). Deletion of a particular in-frame trinucleotide or trinucleotides may not be possible because there. . .

46. 5,122,599, Jun. 16, 1992, CDNAS coding for members of the carcinoembryonic antigen family; Thomas R. Barnett, et al., 536/23.5; 435/6; 536/23.53, 24.31; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,122,599 [IMAGE AVAILABLE] L4: 46 of 90

SUMMARY:

BSUM(35)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

47. 5,116,742, May 26, 1992, RNA ribozyme restriction endoribonucleases and methods; Thomas R. Cech, et al., 435/91.31, 172.3, 199, 320.1; 935/3, 16 [IMAGE AVAILABLE]

US PAT NO: 5,116,742 [IMAGE AVAILABLE] L4: 47 of 90

DETDESC:

DETD(60)

Earlier . . . therein by insertions and deletions to obtain other self-splicing IVS RNA's. In like manner, we could alter the L-19 IVS **RNA** to obtain an **array** of **RNA** sequence-specific endoribonuclease molecules. Thus three regions were found by Price et al. to be necessary for IVS self-splicing. Similar experiments. . .

48. 5,108,892, Apr. 28, 1992, Method of using a TAQ DNA polymerase without 5'-3'-exonuclease activity; Thomas J. Burke, et al., 435/6, 91.2, 91.5, 280, 810; 436/94, 501; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,108,892 [IMAGE AVAILABLE] L4: 48 of 90

DETDESC:

DETD(9)

The term "nucleotide base sequence" is used to describe a linear **array** of nucleotides in a **DNA** molecule commonly made up of four dNTPs: dATP, dCTP, dGTP and dTTP. Modified bases, other than the usual four found. . .

49. 5,102,784, Apr. 7, 1992, Restriction amplification assay; Albert L. George, Jr., 435/6, 194; 436/94, 501; 536/24.3, 25.32 [IMAGE AVAILABLE]

US PAT NO: 5,102,784 [IMAGE AVAILABLE] L4: 49 of 90

SUMMARY:

BSUM(8)

One . . . molecular biology is the ability to fractionate nucleic acids and to determine which nucleic acids have sequences complementary to an **array** of **DNA** or **RNA** molecules. The Southern blot is a well known method for transferring electrophoretically fractioned DNA from a gel matrix to a. . .

50. 5,093,246, Mar. 3, 1992, RNA ribozyme polymerases, dephosphorylases, restriction endoribo-nucleases and methods; Thomas R. Cech, et al., 435/6, 91.31, 194, 258.1, 320.1; 935/3, 16 [IMAGE AVAILABLE]

US PAT NO: 5,093,246 [IMAGE AVAILABLE] L4: 50 of 90

DETDESC:

DETD(54)

Earlier . . . therein by insertions and deletions to obtain other self-splicing IVS RNA's. In like manner, we could alter the L-19 IVS **RNA** to obtain an **array** of **RNA** sequence-specific endoribonuclease molecules. Thus three regions were found by Price et al. to be necessary for IVS self-splicing. Similar experiments. . .

51. 5,082,785, Jan. 21, 1992, Biosynthesis of 2 keto-L-gulonic acid; Ronald F. Manning, et al., 435/252.32, 136, 137, 138, 172.3, 252.3, 320.1; 536/23.2; 935/29, 56, 72 [IMAGE AVAILABLE]

US PAT NO: 5,082,785 [IMAGE AVAILABLE] L4: 51 of 90

DETDESC:

DETD(3)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

52. 5,081,028, Jan. 14, 1992, Preparation of transformed hosts which express binding factor related polypeptides; Hans Hofstetter, et al., 435/172.3, 69.5, 240.2, 252.3, 252.33; 930/140; 935/11, 28, 29, 32, 69,

70, 73 [IMAGE AVAILABLE]

US PAT NO: 5,081,028 [IMAGE AVAILABLE] L4: 52 of 90

DETDESC:

DETD(14)

Available . . . gene and an origin of DNA replication ligated to a portion of the lac Z gene of E. coli. A **DNA** insert containing an **array** of unique restriction enzyme recognation sites has been introduced in the lac Z region of this plasmid.

53. 5,081,019, Jan. 14, 1992, DNA sequences, recombinant DNA molecules and processes for producing lipocortin-like polypeptides; Barbara P. Wallner, et al., 435/69.2, 240.1, 252.3, 320.1; 536/23.2, 23.5, 24.1 [IMAGE AVAILABLE]

US PAT NO: 5,081,019 [IMAGE AVAILABLE] L4: 53 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

54. 5,075,430, Dec. 24, 1991, Process for the purification of DNA on diatomaceous earth; Michael C. Little, 536/25.41; 423/335; 435/803; 536/25.42, 127 [IMAGE AVAILABLE]

US PAT NO: 5,075,430 [IMAGE AVAILABLE] L4: 54 of 90

DETDESC:

DETD(66)

A single-stranded plasmid (M13mp19+strand, 7250 bp) and an **array** or ladder of double-stranded **DNA** (ranging from 2 to 16 Kbp) were each bound to and eluted from Celite following the procedures hereinabove. One .mu.g. . .

55. 5,064,948, Nov. 12, 1991, Chromosome specific repetitive DNA sequences; Robert K. Moyzis, et al., 536/24.31; 435/6; 436/501, 510, 815; 536/23.5; 935/19, 78 [IMAGE AVAILABLE]

US PAT NO: 5,064,948 [IMAGE AVAILABLE] L4: 55 of 90

DETDESC:

DETD(3)

Repetitive . . . of the total DNA of a species, the genome, represented by sequences that are present many times, often in tandem **arrays**. When genomic **DNA** is cut into relatively short fragments and the two strands of the double helix are separated (denatured), the sequences of. . .

56. 5,063,053, Nov. 5, 1991, Isolation and purification of the R18 antigen of HTLV-III; Flossie Wong-Stal, et al., 530/387.9; 435/5; 436/543; 530/350, 389.4; 536/23.72 [IMAGE AVAILABLE]

US PAT NO: 5,063,053 [IMAGE AVAILABLE] L4: 56 of 90

DETDESC:

DETD(19)

CLONING . . . or binding sites, and which contain a marker suitable for identifying the transformed cells (usually tetracycline resistance or ampicillin resistance). **DNA** SEQUENCE: A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

57. 5,047,336, Sep. 10, 1991, DNA sequences, recombinant DNA molecules and processes for producing mullerian inhibiting substance-like polypeptides; Richard L. Cate, et al., 435/69.4, 69.1, 70.1, 71.1, 91.41, 172.1, 172.3, 240.2, 252.3; 536/23.51; 935/29, 32, 34, 38, 56, 57, 60, 66 [IMAGE AVAILABLE]

US PAT NO: 5,047,336 [IMAGE AVAILABLE] L4: 57 of 90

DETDESC:

DETD(4)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

58. 5,045,463, Sep. 3, 1991, DNA expression vector and use thereof; Michael A. Innis, et al., 435/205 [IMAGE AVAILABLE]

US PAT NO: 5,045,463 [IMAGE AVAILABLE] L4: 58 of 90

DETDESC:

DETD(3)

"**DNA** sequence" refers to a linear **array** of nucleotides connected on to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

59. 5,037,746, Aug. 6, 1991, RNA ribozyme polymerases, and methods; Thomas R. Cech, et al., 435/91.31, 90, 172.3, 194, 258.1; 536/23.2, 24.33; 935/3, 16 [IMAGE AVAILABLE]

US PAT NO: 5,037,746 [IMAGE AVAILABLE] L4: 59 of 90

DETDESC:

DETD(57)

Earlier . . . therein by insertions and deletions to obtain other self-splicing IVS RNA's. In like manner, we could alter the L-19 IVS **RNA** to obtain an **array** of **RNA** sequence-specific endoribonuclease molecules. Thus three regions were found by Price et al. to be necessary for IVS self-splicing. Similar experiments. . .

60. 5,021,342, Jun. 4, 1991, Expression cDNA clones encoding antigens of onchocerca volvulus; Bruce M. Greene, et al., 435/252.33, 69.1, 172.3, 320.1; 530/350; 536/23.7; 935/18, 31, 47, 58, 65, 73, 81 [IMAGE AVAILABLE]

US PAT NO: 5,021,342 [IMAGE AVAILABLE] L4: 60 of 90

SUMMARY:

BSUM(10)

DNA Sequence - A linear **array** of nucleotides connected one to the other by phosphodiester bonds between 3' and 5' carbons of adjacent pentoses.

61. 5,004,689, Apr. 2, 1991, DNA sequences, recombinant DNA molecules and processes for producing human gamma interferon-like polypeptides in high yields; Walter C. Fiers, et al., 435/69.51, 252.3, 252.33, 320.1; 935/11, 44, 46, 73 [IMAGE AVAILABLE]

US PAT NO: 5,004,689 [IMAGE AVAILABLE] L4: 61 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

62. 4,989,113, Jan. 29, 1991, Data processing device having direct memory access with improved transfer control; Kim Asal, 395/425; 364/242.3, 242.31, 242.32, 242.33, 247, 247.8, DIG.1; 395/725 [IMAGE AVAILABLE]

US PAT NO: 4,989,113 [IMAGE AVAILABLE] L4: 62 of 90

ABSTRACT:
A microcomputer is disclosed which provides for a dedicated DMA data and address bus connecting an on-**chip** **DNA** controller with on-**chip** memories, and with on-chip ports for access to external memory and input/output devices. The DMA controller contains a control register. . .

63. 4,987,071, Jan. 22, 1991, RNA ribozyme polymerases, dephosphorylases, restriction endoribonucleases and methods; Thomas R. Cech, et al., 435/91.31, 172.3, 193, 194; 502/167; 536/23.1, 24.1; 935/3, 14 [IMAGE AVAILABLE]

US PAT NO: 4,987,071 [IMAGE AVAILABLE] L4: 63 of 90

DETDESC:

DETD(54)

Earlier . . . therein by insertions and deletions to obtain other self-splicing IVS RNA's. In like manner, we could alter the L-19 IVS **RNA** to obtain an **array** of **RNA** sequence-specific endoribonuclease molecules. Thus three regions were found by Price et al. to be necessary for IVS self-splicing. Similar experiments. . .

64. 4,981,783, Jan. 1, 1991, Method for detecting pathological conditions; Leonard Augenlicht, 435/6, 803; 436/501, 813; 935/3, 9, 19, 29, 78, 80 [IMAGE AVAILABLE]

US PAT NO: 4,981,783 [IMAGE AVAILABLE] L4: 64 of 90

DETDESC:

DETD(47)

Replica . . . would be made from each of the selected clones, the DNA denatured, and deposited in uniform spots in a patterned **array**, individually spotting the **DNA**, or by using any one of several available devices made for this purpose. The use of purified DNA will produce. . .

65. 4,963,497, Oct. 16, 1990, Isolation and purification of the eighth gene of HTLV-III; Flossie Wong-Staal, et al., 435/320.1, 172.3; 536/23.72, 24.1 [IMAGE AVAILABLE]

US PAT NO: 4,963,497 [IMAGE AVAILABLE] L4: 65 of 90

DETDESC:

DETD(21)

DNA SEQUENCE: A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

66. 4,950,646, Aug. 21, 1990, DNA sequences, recombinant DNA molecules and processes for producing human lipocortin-like polypeptides; Barbara P. Wallner, et al., 514/12, 350 [IMAGE AVAILABLE]

US PAT NO: 4,950,646 [IMAGE AVAILABLE] L4: 66 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

67. 4,898,828, Feb. 6, 1990, Ultrahigh copy number streptomycetes plasmids; Charles L. Hershberger, et al., 435/252.3, 172.3, 252.33, 252.35, 320.1; 536/24.1; 935/6, 29, 73, 75 [IMAGE AVAILABLE]

US PAT NO: 4,898,828 [IMAGE AVAILABLE] L4: 67 of 90

DETDESC:

DETD(12)

Plasmid . . . of SCP2* and identify the sequences that are essential for plasmid replication. Partial digestion of pHJL192 with KpnI generated an **array** of linear products and T4 **DNA** ligase formed circular molecules that transformed E. coli K12 C600R.sub.k --M.sub.k --to ampicillin resistance. Restriction mapping identified the plasmids pHJL200-205.. . .

68. 4,886,753, Dec. 12, 1989, Method for the expression of genes in plants, parts of plants, and plant cell cultures, and DNA fragments, plasmids, and transformed microorganisms to be used when carrying out the method, as well as the use thereof for the expression of genes in plants; Kjeld A. Marcker, et al., 435/172.3; 536/23.6; 935/35, 41, 43, 67 [IMAGE AVAILABLE]

US PAT NO: 4,886,753 [IMAGE AVAILABLE] L4: 68 of 90

SUMMARY:

BSUM(13)

DNA sequence or **DNA** segment: A linear **array** of nucleotides interconnected through phosphodiester bonds between the 3' and 5' carbon atoms of adjacent pentoses.

69. 4,879,224, Nov. 7, 1989, DNA sequences, recombinant DNA molecules and processes for producing human phospholipase inhibitor polypeptides; Barbara P. Wallner, et al., 435/68.1, 240.2, 240.4, 252.31, 252.33, 252.34, 252.35, 254.11, 254.2, 320.1; 536/23.2; 935/11, 27, 31, 72 [IMAGE AVAILABLE]

US PAT NO: 4,879,224 [IMAGE AVAILABLE] L4: 69 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

70. 4,874,743, Oct. 17, 1989, DNA sequences, recombinant DNA molecules and processes for producing human phospholipase inhibitor-like polypeptides; Barbara P. Wallner, et al., 514/12; 530/350 [IMAGE AVAILABLE]

US PAT NO: 4,874,743 [IMAGE AVAILABLE] L4: 70 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

71. 4,874,702, Oct. 17, 1989, Vectors and methods for making such vectors and for expressive cloned genes; Walter C. Fiers, et al., 435/172.3, 69.3, 69.4, 69.51, 172.1, 252.3, 252.33, 320.1; 536/23.2, 23.5, 23.51, 23.52, 24.1, 24.2; 935/39, 40, 41, 44, 45 [IMAGE AVAILABLE]

US PAT NO: 4,874,702 [IMAGE AVAILABLE] L4: 71 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

72. 4,863,849, Sep. 5, 1989, Automatable process for sequencing nucleotide; Robert J. Melamede, 435/6, 91.3, 91.5, 91.51; 935/77, 78, 88 [IMAGE AVAILABLE]

US PAT NO: 4,863,849 [IMAGE AVAILABLE] L4: 72 of 90

SUMMARY:

BSUM(39)
(b) a method for producing from this population of radioactive **polynucleotides** an **array** of **polynucleotides** with one common terminus but varying in length at the other terminus in increments of a single base; and

73. 4,849,348, Jul. 18, 1989, Post-transcriptional heme regulated heterologous gene expression in yeast using the leg hemoglobin leader sequence; Kjeld A. Marcker, et al., 435/69.1, 91.41, 172.3, 193, 254.21, 320.1; 536/23.1, 23.5, 23.6, 24.1, 24.2; 935/28, 37, 56, 69 [IMAGE AVAILABLE]

US PAT NO: 4,849,348 [IMAGE AVAILABLE] L4: 73 of 90

SUMMARY:

BSUM(9)

DNA sequence or **DNA** segment: A linear **array** of nucleotides interconnected through phosphodiester bonds between the 3' and 5' carbon atoms of adjacent pentoses.

74. 4,794,175, Dec. 27, 1988, Glucoamylase CDNA; Jack Nunberg, et al., 536/24.3; 435/91.51, 91.53, 172.1, 172.3, 205, 254.3, 320.1, 914; 536/23.2, 23.7, 24.32; 935/14, 19, 21, 29, 68, 72, 73 [IMAGE AVAILABLE]

US PAT NO: 4,794,175 [IMAGE AVAILABLE] L4: 74 of 90

DETDESC:

DETD(3)

"**DNA** sequence" refers to a linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

75. 4,758,512, Jul. 19, 1988, Hosts and methods for producing recombinant products in high yields; Alfred L. Goldberg, et al., 435/69.3, 69.4, 69.51, 172.1, 172.3, 839, 849; 935/16, 72, 73, 74 [IMAGE AVAILABLE]

US PAT NO: 4,758,512 [IMAGE AVAILABLE] L4: 75 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

76. 4,731,325, Mar. 15, 1988, Arrays of alternating nucleic acid fragments for hybridization arrays; Airi M. Palva, et al., 435/6, 5, 91.41, 91.52; 436/501; 536/24.3, 24.32; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 4,731,325 [IMAGE AVAILABLE] L4: 76 of 90

DETDESC:

DETD(56)

The . . . other hand, hybridization with a reagent of b.sub.1, b.sub.2 or b.sub.1, b.sub.2, b.sub.3 detects as few as 10.sup.6 molecules of CMV-**DNA**. The results show that the **array** of nucleic acid reagents are four times as sensitive as individual nucleic acid reagents.

77. 4,729,954, Mar. 8, 1988, pLS010 plasmid vector; Sanford A. Lacks, et al., 435/172.3, 320.1; 935/22, 29 [IMAGE AVAILABLE]

US PAT NO: 4,729,954 [IMAGE AVAILABLE] L4: 77 of 90

DETDESC:

DETD(21)

The . . . digest to a linearized and phosphatase treated vector results in the generation of hemiligated recombinant plasmid molecules (FIG. 3, middle **array**). Because the chromosomal **DNA** fragments were heterogeneous, the recombinant molecules generally contain different inserts. However, the pre-existing nicks in the hemiligated molecule result in. . .

DETDESC:

DETD(23)

In . . . because two fragments that are complementary at the junction regions are likely to enter the same cell (FIG. 3, lowest **array**). To examine this, SV40 **DNA** was linearized with HpaII and ligated to phosphatase treated pLS101 which had also been linearized with HpaII. On transforming strain. . .

78. 4,716,112, Dec. 29, 1987, Vectors for increased expression of cloned genes; Nikos Panayotatos, 435/69.1, 69.2, 69.3, 69.51, 69.6, 172.3, 320.1; 536/23.1, 24.1; 935/29, 41, 42, 60 [IMAGE AVAILABLE]

US PAT NO: 4,716,112 [IMAGE AVAILABLE] L4: 78 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

79. 4,693,973, Sep. 15, 1987, DNA sequences, recombinant DNA molecules and processes for producing bovine growth hormone-like polypeptides in high yield; Gary N. Buell, 435/69.4, 172.3; 530/399; 930/120, 300 [IMAGE AVAILABLE]

US PAT NO: 4,693,973 [IMAGE AVAILABLE] L4: 79 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

80. 4,686,184, Aug. 11, 1987, Gene transfer vector; Alfred Puhler, et al., 435/172.3, 252.2, 252.33, 320.1, 878; 536/23.1, 24.1; 935/27 [IMAGE AVAILABLE]

US PAT NO: 4,686,184 [IMAGE AVAILABLE] L4: 80 of 90

SUMMARY:

BSUM(2)

The . . . of a vast store of detailed, basic knowledge of the genetics of Escherichia coli (hereinafter "E. coli") and an extensive **array** of **DNA** vectors, plasmids, and phages specifically developed

with the aid of such knowledge for use in E. coli. Although E. coli. . .

81. 4,675,283, Jun. 23, 1987, Detection and isolation of homologous, repeated and amplified nucleic acid sequences; Igor Roninson, 435/6; 204/182.8; 435/18, 91.41, 803; 436/501; 536/24.3; 935/76, 77, 78 [IMAGE AVAILABLE]

US PAT NO: 4,675,283 [IMAGE AVAILABLE] L4: 81 of 90

SUMMARY:

BSUM(4)

Much . . . copy sequences. In the second type of arrangement, the basic structural units are linked to each other in long tandem **arrays**. When total genomic **DNA** is digested with a restriction enzyme, that disrupts DNA at specific sites, the interspersed repeated sequences give rise to a. . .

82. 4,626,504, Dec. 2, 1986, DNA transfer vector for gram-negative bacteria; Alfred Puhler, et al., 435/172.3, 252.2, 252.3, 252.33, 320.1; 536/23.1; 935/29, 30, 55, 67, 72 [IMAGE AVAILABLE]

US PAT NO: 4,626,504 [IMAGE AVAILABLE] L4: 82 of 90

SUMMARY:

BSUM(3)

The . . . of a vast store of detailed, basic knowledge of the genetics of Escherichia coli (hereinafter "E. coli") and an extensive **array** of **DNA** vectors, plasmids, and phages specifically developed with the aid of such knowledge for use in E. coli. Although E. coli. . .

83. 4,591,567, May 27, 1986, Recombinant **DNA** screening system including fixed **array** replicator and support; Roy J. Britten, et al., 435/293, 5, 6, 30, 292, 800, 809; 935/80, 86 [IMAGE AVAILABLE]

US PAT NO: 4,591,567 [IMAGE AVAILABLE] L4: 83 of 90
TITLE: Recombinant **DNA** screening system including fixed **array** replicator and support

ABSTRACT:
A system for the production and maintenance of genomic libraries of recombinant **DNA** in a fixed geometric **array** arranged so that such libraries may be accurately replicated and maintained with the same set of individual DNA inserts occupying. . .

SUMMARY:

BSUM(16)

Briefly . . . present invention comprehends a system for the production and maintenance of genomic libraries and maintenance of genomic libraries of recombinant **DNA** in a fixed geometric **array** arranged so that such libraries may be accurately replicated and maintained with the same set of individual DNA inserts occupying. . .

DETDESC:

DETD(8)

This . . . all of the sequences in a mammalian genome, and each insert will be located at a fixed "address" in the **array**. After **DNA** transfer from the **array** to a filter and hybridization with a highly labeled probe, the radioactivity is detected by simultaneous large area direct counting. . .

84. 4,553,351, Nov. 19, 1985, Method of treating a soil; R. Edgar Guay, 47/58, 9; 71/11; 111/118, 900 [IMAGE AVAILABLE]

US PAT NO: 4,553,351 [IMAGE AVAILABLE] L4: 84 of 90

SUMMARY:

BSUM(35)

Because . . . of the present invention, it is possible to add to the soil not only organic matter but also an interesting **array** of **oligo** elements and thus avoid loss of crops because of the time lost by fallowing to which some farmers must presently. . .

85. 4,530,901, Jul. 23, 1985, Recombinant DNA molecules and their use in producing human interferon-like polypeptides; Charles Weissmann, 435/69.51, 91.41, 172.3, 240.26, 252.3, 252.31, 252.33, 252.34, 254.11, 254.2, 320.1, 811, 832, 839, 849; 536/23.52, 24.1; 930/10, 240; 935/11, 18, 29, 60, 67, 68, 69, 70, 72, 73 [IMAGE AVAILABLE]

US PAT NO: 4,530,901 [IMAGE AVAILABLE] L4: 85 of 90

DETDESC:

DETD(5)

DNA Sequence--A linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

86. 4,416,988, Nov. 22, 1983, Detection and isolation of enkephalin mRNA using a synthetic oligodeoxynucleotide; Harvey Rubin, 435/91.51, 6; 436/63, 94; 536/23.1, 23.51, 24.3, 24.31; 930/80 [IMAGE AVAILABLE]

US PAT NO: 4,416,988 [IMAGE AVAILABLE] L4: 86 of 90

DETDESC:

DETD(10)

The . . . plus 15-mer by the technique described in N. Davidson, Biochemistry 17, 3883 (1978). The 15-mer is then complexed to DBM **chips** and A+ **RNA** from brain, pancreas, adrenal, medula or pituitary is hybridized to the 15-mer immobilized on the chips by the procedure described. . .

87. 4,358,586, Nov. 9, 1982, Detection and isolation of endorphin mRNA using a synthetic oligodeoxynucleotide; Harvey Rubin, 536/24.31; 435/6, 172.3; 536/24.33, 25.3, 25.32, 30; 930/80; 935/2, 8, 18, 21, 78 [IMAGE AVAILABLE]

US PAT NO: 4,358,586 [IMAGE AVAILABLE] L4: 87 of 90

DETDESC:

DETD(10)

The . . . plus 15-mer by the technique described in N. Davidson, Biochemistry 17, 3883 (1978). The 15-mer is then complexed to DBM **chips** and A+ **RNA** from brain, pancreas, adrenal, medula or pituitary is hybridized to the 15-mer immobilized on the chips by the procedure described. . .

88. 4,089,051, May 9, 1978, Alternative direct and indirect addressing; James P. Lee, Jr., et al., 395/425; 364/238.5, 239, 239.3, 239.7, 240.1, 241.2, 242.2, 242.3, 254, 254.2, 255, 255.1, 255.4, 259, 259.4, 262.4, 262.6, DIG.1 [IMAGE AVAILABLE]

US PAT NO: 4,089,051 [IMAGE AVAILABLE] L4: 88 of 90

DETDESC:

DETD(9)

Units D1A through **DNA** may constitute circuit **chips** or portions thereof that advantageously provide the various functions of a modem. For example, input unit 111 might translate incoming. . .

89. 3,854,223, Dec. 17, 1974, MOLECULAR MODELS FOR NUCLEIC ACIDS; Charles Wesley Dingman, II, 434/278; 446/92 [IMAGE AVAILABLE]

US PAT NO: 3,854,223 [IMAGE AVAILABLE] L4: 89 of 90

DRAWING DESC:

DRWD(12)

FIG. . . . blocks. These gaps enable the user to insert structures (representing, for example, drugs which intercalate between nucleotide pairs of double-stranded **polynucleotides**) between blocks in vertical **arrays**, and to remove the spring clip connecting selected pairs of blocks contained within long vertical, `double-stranded,` arrays to represent localized. . .

90. 3,802,097, Apr. 9, 1974, DNA MODEL KIT; Alfred I. Gluck, 434/279 [IMAGE AVAILABLE]

US PAT NO: 3,802,097 [IMAGE AVAILABLE] L4: 90 of 90

SUMMARY:

BSUM(8)

The kit is particularly intended for constructing a DNA (deoxyribonucleic acid) molecule, in which case the plurality of groups of **chips** designate components of the **DNA** molecule and include a group of S-chips each designating the sugar chain, a group of P-chips each designating the phosphate. . .

DRAWING DESC:

DRWD(3)

FIG. 1 illustrates one chip of each of the component groups used in constructing the **DNA** molecule; namely an S-**chip** designating the sugar chain; a P-chip designating the phosphate chain; a T-chip designating the thymine base; a C-chip designating the. . .

DRAWING DESC:

DRWD(5)

FIG. 3 illustrates the use of the foregoing **chips** in constructing a **DNA** molecule;

CLAIMS:

CLMS(5)

5. A kit as defined in claim 1 for constructing a DNA (deoxyribonucleic acid) molecule, wherein said plurality of groups of **chips** designate components of the **DNA** molecule and include a group of S-chips each designating the sugar chain, a group of P-chips each designating the phosphate. . .

=>

1. 5,436,389, Jul. 25, 1995, Hybrid genetic complement and corn plant DK570; John H. Pfund, 800/200; 435/240.4, 240.49, 240.5; 800/250, DIG.56 [IMAGE AVAILABLE]

US PAT NO: 5,436,389 [IMAGE AVAILABLE] L8: 1 of 78

SUMMARY:

BSUM(47)

Probes were prepared to the fragment **sequences**, these probes being complementary to the **sequences** thereby being capable of hybridizing to them under appropriate conditions well known to those skilled in the art. These probes. . . of detection. After the fragments are separated by size, they were identified by the probes. Hybridization with a unique cloned **sequence** permits the identification of a specific chromosomal region (locus). Because all alleles at a locus are detectable, RFLP's are codominant. . . a genetic marker. They differ from some other types of markers, e.g, from isozymes, in that they reflect the primary **DNA** **sequence**, they are not products of transcription or translation. Furthermore, different RFLP profiles result from different **arrays** of restriction endonucleases.

2. 5,428,147, Jun. 27, 1995, Octopine T-DNA promoters; Richard F. Barker, et al., 536/24.1; 435/69.1, 70.1, 172.3, 240.4, 252.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,428,147 [IMAGE AVAILABLE] L8: 2 of 78

SUMMARY:

BSUM(39)

In contrast to the situation in octopine-type tumors, nopaline T-**DNA** is integrated into the host genome in one continuous fragment (M. Lemmers et al. (1980) J. Mol. Biol. 144:353-376, P. Zambryski et al. (1980) Science 209:1385-1391). Direct tandem repeats were observed. T-**DNA** of plants regenerated from teratomas had minor modifications in the border fragments of the inserted **DNA** (Lemmers et al., supra). **Sequence** analysis of the junction between the right and left borders revealed a number of direct repeats and one inverted repeat.. . . single nucleotide (P. Zambryski et al. (1982) J. Mol. Appl. Genet. 1:361-370). Left and right borders in junctions of tandem **arrays** were separated by spacers which could be over 130 bp. The spacers were of unknown origin and contained some T-**DNA** **sequences**. T-**DNA** was found to be integrated into both repeated and low copy number host **sequences**. H. Joos et al. (1983) Cell 32:1057-1067, have shown that virulence is not eliminated after deletion of either of the usual nopaline T-**DNA**

borders.

3. 5,427,932, Jun. 27, 1995, Repeat sequence chromosome specific nucleic acid probes and methods of preparing and using; Heinz-Ulrich G. Weier, et al., 435/91.2, 6, 810; 436/501; 536/22.1, 23.1, 24.3, 24.31, 24.33; 935/78, 88 [IMAGE AVAILABLE]

US PAT NO: 5,427,932 [IMAGE AVAILABLE] L8: 3 of 78

DETDESC:

DETD(145)

In Examples 1 and2, it is shown that centromeric repeated **DNA** can be selectively amplified using a pair of degenerate alpha satellite consensus primers. PCR reproduces naturally occurring variations in the base **sequences** between primer annealing sites by using **oligonucleotide** primers that anneal in the most conserved parts of the alphoid monomer repeat. The resulting probe **DNA** is a heterogeneous mixture of **DNA** fragments in different size ranges with a variety of nucleotide **sequences**. The degeneracy of the PCR-generated probe **DNA** may be advantageous during in situ hybridization compared to the use of conventional clonal **DNA** probes, because it allows deposition of a very dense **array** of probes along the chromosomal target.

4. 5,427,911, Jun. 27, 1995, Coupled amplification and sequencing of DNA; Gualberto Ruano, 435/6, 91.2; 536/24.33 [IMAGE AVAILABLE]

US PAT NO: 5,427,911 [IMAGE AVAILABLE] L8: 4 of 78

DETDESC:

DETD(3)

The . . . allows 10,000 to 100,000-fold amplification of a genomic segment of 1 kb or less starting from .mu.g amounts of genomic **DNA**. At the beginning of Stage II, 8 of 10 identical aliquots of Stage I product are set aside. Each aliquot receives one of the 4 dideoxynucleotides and a radiolabelled supplement of one of the two PCR primers. Hence five **sequencing** reactions from each end of the PCR fragment are set in the **array** of ten aliquots (two are controls). These ten **sequencing** reactions are thermally cycled during Stage II to simultaneously amplify both the template and the truncated products giving rise to two **sequencing** ladders on a polyacrylamide gel. The **sequencing** ladders are complementary, since each starts at opposite 5' ends of the PCR fragment. Concentrations of deoxynucleotides, of dideoxynucleotides and. . .

5. 5,426,041, Jun. 20, 1995, Binary cryptocytotoxic method of hybrid seed production; Steven F. Fabijanski, et al., 435/172.3; 47/58, DIG.1; 800/205; 935/35, 59 [IMAGE AVAILABLE]

US PAT NO: 5,426,041 [IMAGE AVAILABLE] L8: 5 of 78

DETDESC:

DETD(91)

This . . . pPAL 889. pPAL 889 was digested with Eco RI, and briefly treated with Exonuclease III, followed by S1 nuclease. The **DNA** was digested with Sma I and treated with Klenow fragment to make it blunt ended. The **DNA** was relegated and clones recovered. Some of these clones were chosen, **sequenced**, and one clone was found which had 5'

sequences deleted such that only approximate 15 bases upstream of the ATG start of translation codon remained. This plasmid was named. . . fragment. This plasmid was named pPAL 887. This plasmid contains the promoterless version of the lamS gene and contains the **array** of restriction sites shown that flank the gene as shown in FIG. 3.

6. 5,424,483, Jun. 13, 1995, Methods and compositions of a hybrid genetic corn complement, DK554; John H. Pfund, et al., 800/200; 435/240.4; 800/250, DIG.56 [IMAGE AVAILABLE]

US PAT NO: 5,424,483 [IMAGE AVAILABLE] L8: 6 of 78

SUMMARY:

BSUM(52)

Probes were prepared to the fragment **sequences**, these probes being complementary to the **sequences** thereby being capable of hybridizing to them under appropriate conditions well known to those skilled in the art. These probes. . . of detection. After the fragments are separated by size, they were identified by the probes. Hybridization with a unique cloned **sequence** permits the identification of a specific chromosomal region (locus). Because all alleles at a locus are detectable, RFLP's are codominant. . . a genetic marker. They differ from some other types of markers, e.g, from isozymes, in that they reflect the primary **DNA** **sequence**, they are not products of transcription or translation. Furthermore, different RFLP profiles result from different **arrays** of restriction endonucleases.

7. 5,420,019, May 30, 1995, Stable bactericidal/permeability-increasing protein muteins; Georgia Theofan, et al., 435/69.1, 252.3, 320.1; 530/350; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,420,019 [IMAGE AVAILABLE] L8: 7 of 78

SUMMARY:

BSUM(9)

Even . . . For example, it is difficult to detect full-length expression product in a medium containing host cells transformed or transfected with **DNA** encoding rBPI(1-199). Instead, the expression products obtained from such cells represent an heterogeneous **array** of carboxy-terminal truncated species of the rBPI N-terminal fragment. In fact, the expected full-length product (1-199) is often not detected as being among the rBPI species present in that heterogeneous **array**. Heterogeneity of the carboxy terminal amino acid **sequence** of rBPI(1-199) products appears to result from activity of carboxypeptidases in host cell cytoplasm and/or culture supernatant.

8. 5,410,652, Apr. 25, 1995, Data communication control by arbitrating for a data transfer control token with facilities for halting a data transfer by maintaining possession of the token; Jerald G. Leach, et al., 395/250; 364/239.7, 242.6, DIG.1; 395/725 [IMAGE AVAILABLE]

US PAT NO: 5,410,652 [IMAGE AVAILABLE] L8: 8 of 78

DETDESC:

DETD(104)

TABLE 4

DNA Channel Control Register
Bit Position
Bit Definition

0-1 **DNA** PRI
DMA PRIority. Defines the arbitration rules to be used when a DMA channel and the CPU are. . . channel in split mode only.
It is useful to keep the link pointer constant when autoinitializing from the on-**chip** com ports of other stream oriented devices such a FIFOs.
10 AUTOINIT
If AUTO INIT SYNCH = 0. . . The START and AUX START bits, if used to hold a
channel in the middle of an autoinitialization **sequence**, will hold the autoinitialization **sequence**. If the START or AUX START bits are being modified by the DMA channel (for example, to force. . .

9. 5,409,700, Apr. 25, 1995, Pharmaceutical compositions comprising modified and unmodified plasminogen activators; Jutta Heim, et al., 424/94.64, 94.63; 435/212, 215; 514/2 [IMAGE AVAILABLE]

US PAT NO: 5,409,700 [IMAGE AVAILABLE] L8: 9 of 78

DETDESC:

DETD(5)

Plasmid . . . Biol. 4, 2668-2675) contains the yeast genes for the repressible and constitutive acid phosphatases (PH05 and PH03) in a tandem **array** on a 3,9 kb BamHI-HpaI fragment (Bajwa et al. (1984), Nucleic Acids Research 12, 7721-7739). The **DNA** fragment is isolated from plasmid p30 (European Patent Application No. 143 081, deposited as DSM 4297) and cloned in pBR322. . . BamHI and PvuII in clockwise orientation, which results in plasmid p29. An AccI restriction digest, a fill-in reaction with Klenow **DNA** polymerase and a BamHI restriction digest leads to a 626 bp fragment that contains the PH05 promoter, signal **sequence** and a 34 nucleotide extension into the coding **sequence** of mature PH05.

10. 5,405,938, Apr. 11, 1995, Sequence-specific binding polymers for duplex nucleic acids; James E. Summerton, et al., 528/406; 525/54.2, 54.3, 383, 384, 385; 528/245, 403, 417, 420, 422, 423, 425 [IMAGE AVAILABLE]

US PAT NO: 5,405,938 [IMAGE AVAILABLE] L8: 10 of 78

SUMMARY:

BSUM(133)

Also . . . part of the invention is a subunit composition for use in forming a polymer composition effective to bind in a **sequence** specific manner to a target **sequence** in a duplex **polynucleotide**. The composition includes one of the following subunit structures: ##STR9## where R' is H, OH, or O-alkyl; the 5'-methylene has. . . stereochemical orientation, is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the aliphatic backbone moiety: ##STR10## where the * ring position may carry a hydrogen-bond acceptor group; and. . . where R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen

bonding **arrays**, where B indicates the aliphatic backbone moiety: ##STR11## where the * ring position may carry a hydrogen-bond donating group; and. . .

SUMMARY:

BSUM(134)

An . . . part of the invention is a subunit composition for use in forming a polymer composition effective to bind in a **sequence** specific manner to a target **sequence** in a duplex **polynucleotide**. The composition includes one of the following subunit structures: ##STR12## where the 5'-methylene has a .beta. stereochemical orientation in subunit. . . stereochemical orientation, is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the aliphatic backbone moiety, the starred atom is not a hydrogen bond acceptor, and W is oxygen. . .

CLAIMS:

CLMS(1)

It is claimed:

1. A polymer composition effective to bind in a **sequence**-specific manner to a target **sequence** of a duplex **polynucleotide** containing at least two different-oriented Watson/Crick base-pairs at selected positions in the target **sequence**, comprising a specific **sequence** of subunits having the form: ##STR16## where Y is a 2- or 3-atom length, uncharged intersubunit linkage group; R' is. . .
base-pair, R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR17## where the * ring position may carry a hydrogen-bond donor group, such as. . . base-pair, R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR18## where the * ring position may carry a hydrogen-bond acceptor group, such as. . . base-pair, R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR19## where the * ring position may carry a hydrogen-bond acceptor group, such as. . . base-pair, R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR20## where the * ring position may carry a hydrogen-bond donating group, such as. . .

CLAIMS:

CLMS(22)

22. A subunit composition for use in forming a polymer composition effective to bind in a **sequence** specific manner to a target **sequence** in a duplex **polynucleotide**, comprising one of the following subunit structures: ##STR36## where R' is H, OH, or O-alkyl; the 5'-methylene has a .beta.. . . stereochemical orientation, is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the aliphatic backbone moiety: ##STR37## where the * ring position may carry a hydrogen-bond acceptor group; and. . . where R.sub.i is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where

B indicates the aliphatic backbone moiety: ##STR38## where the * ring position may carry a hydrogen-bond donating group; and. . .

CLAIMS:

CLMS(23)

23. A subunit composition for use in forming a polymer composition effective to bind in a **sequence** specific manner to a target **sequence** in a duplex **polynucleotide**, comprising one of the following subunit structures: ##STR39## where the 5'-methylene has a .beta. stereochemical orientation in subunit forms (b),. . . stereochemical orientation, is selected from the group consisting of planar bases having the following skeletal ring structures and hydrogen bonding **arrays**, where B indicates the aliphatic backbone moiety, the starred atom is not a hydrogen bond acceptor, and W is oxygen. . .

11. 5,374,517, Dec. 20, 1994, IM peptides; Tom B. Sculley, et al., 435/5, 7.95, 975; 436/812; 530/325, 326, 329 [IMAGE AVAILABLE]

US PAT NO: 5,374,517 [IMAGE AVAILABLE] L8: 11 of 78

SUMMARY:

BSUM(13)

Antibodies can be used to determine whether an ORF present in a **DNA** **sequence** codes for a protein. This involves manufacturing an **array** of protein fragments or synthetic polypeptides whose amino acid residue **sequences** correspond to the hypothetical **sequences** obtained from the ORFs. The protein fragments or polypeptides to which naturally occurring antibodies immunoreact thereby identify the ORF as encoding a naturally occurring protein. The complete amino acid **sequence** of this protein could then be deduced from the **DNA** **sequence** of the ORF.

12. 5,366,887, Nov. 22, 1994, RI T-DNA promoters; Jerry L. Slightom, et al., 435/240.4, 172.3, 240.1, 320.1; 536/23.1, 24.1; 935/6, 35, 56 [IMAGE AVAILABLE]

US PAT NO: 5,366,887 [IMAGE AVAILABLE] L8: 12 of 78

SUMMARY:

BSUM(33)

A portion of the Ti or Ri plasmid is found in the **DNA** of tumorous plant cells, T-**DNA** may be integrated (i,e. inserted) into host **DNA** at multiple sites in the nucleus, Flanking plant **DNA** may be either repeated or low copy number **sequences**, Integrated T-**DNA** can be found in either direct or inverted tandem **arrays** and can be separated by spacers, Much non-T-**DNA** Ti plasmid **DNA** appears to be transferred into the plant cell prior to T-**DNA** integration (H, Joos et al, (1983) EMBO J. 2:2151-2160). T-**DNA** has direct repeats of about 25 base pairs associated with the borders, i.e. with the T-**DNA**/plant **DNA** junctions, which may be involved in either transfer from Agrobacterium or integration into the host genome.

13. 5,366,874, Nov. 22, 1994, Molecular cloning and expression of biologically-active diphtheria toxin receptor; Leon Eidels, et al., 435/69.1, 7.1, 7.2, 252.3, 320.1; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,366,874 [IMAGE AVAILABLE] L8: 13 of 78

DETDESC:

DETD(35)

To confirm that these DT.sup.S -I mouse cells contain Vero cell cDNA, Southern blotting analysis was performed. **DNA** from these cells was digested with an **array** of restriction enzymes, separated on an agarose gel, transferred to a nylon membrane, and probed with a [.sup.32 P]-labeled cytomegalovirus immediate early-promoter **DNA** **sequence** (Thomsen et al., 1984) under very stringent hybridization conditions (described in the Methods section). The **DNA** hybridization pattern obtained revealed that these cells contained vector **sequences**, a result consistent with the interpretation that the observed DT sensitivity phenotype was most likely due to the presence of. . .

14. 5,352,607, Oct. 4, 1994, Molecular clone of a chitinase gene from vibrio parahemolyticus; Roger A. Laine, et al., 435/252.33, 172.3, 220, 320.1, 909; 536/23.2, 23.7 [IMAGE AVAILABLE]

US PAT NO: 5,352,607 [IMAGE AVAILABLE] L8: 14 of 78

DETDESC:

DETD(5)

Chromosomal **DNA** of Vibrio parahemolyticus was digested with restriction endonucleases according to manufacturer's recommendations. **DNA** was electrophoresed in an agarose gel and transferred onto a nitrocellulose filter, hybridized with a nick-translated **DNA** probe as described previously by C. Y. Ou et al. in "A novel **sequence** segment and other nucleotide structural features in the long terminal repeat of a BALB/c mouse genomic leukemia virus-related **DNA** clone. Nucleic Acid Research. 11: 5603-5620. Nick-translated pC139 **DNA** was prepared according to P. Rigby et al. in "Labeling deoxynucleic acids to high specific activity in vitro by nick-translation with **DNA** polymerase", I. J. Mol. Biol. 113:237-251, and had a specific activity of 2.times.10 cpm/ug. To demonstrate that the pC139 plasmid. . . Hcl, pH 7.5, 10 mM EDTA). These total cell extracts were centrifuged at 25,000.times.g for 60 minutes to remove chromosomal **DNA** and were dialyzed against KP buffer. The presence of lysozyme in the enzyme preparation did not interfere with the detection. . . an 804 medium, supplemented with 0.5% (w/v) swollen chitin. The production of chitinase was judged by the disappearance of chitin **chips** in the medium. After the complete disappearance of chitin (usually 36-48 hours at 37.degree. C.), the medium was collected, concentrated. . . 3 weeks, and were then bled with the anti-chitinase titer reached 1:16 as judged by Ouchterlony double diffusion. The plasmid **DNA**, designated pC139, from this E. coli was isolated and shown to have 5.9 kbp Vibrio **DNA** insert. A restriction enzyme map was constructed and shown in FIG. 1. Nick-translated pC139 **DNA** hybridized with a 3.7 kbp EcoR-I fragment and a 0.7 kbp. Hind-III **DNA** fragments (FIG. 2) which was predicted by the restriction map of pC139. Since the chromosomal Vibrio **DNA** used for the construction of the plasmid library was partially digested with Sau3A enzyme, it was possible that some of. . . other EcoR-I fragments, and two other Hind-III fragments (larger that 9 kbp, and 3.2 kbp) which appear to be the **sequences** flanking the 3.7 kbp EcoR-I and 0.7 kbp Hind-III internal segments, respectively. There is only one segment each for BamH-I,. . . fragments detected by the pC139 probe. These results strongly suggested that most, if not all, of the 5.0 kbp insert **DNA** was derived from one continuous segment from the chromosomal **DNA**.

15. 5,342,774, Aug. 30, 1994, Nucleotide sequence encoding the tumor rejection antigen precursor, MAGE-1; Thierry Boon, et al., 435/240.2,

69.1, 69.3, 172.3, 235.1, 252.3, 320.1; 530/350; 536/23.5; 935/9, 32, 34, 57, 62, 70, 71 [IMAGE AVAILABLE]

US PAT NO: 5,342,774 [IMAGE AVAILABLE] L8: 15 of 78

DETDESC:

DETD(103)

In . . . third exon. In contrast with the result observed with human tumor cell line MZ2-MEL 3.0, no band was observed with **RNA** isolated from a CTL clone of patient MZ2 and phytohemagglutinin-activated blood lymphocytes of the same patient. Also negative were several. . . provided no clear indication as to which of genes mage-1, 2 or 3 were expressed by these cells, because the **DNA** probes corresponding to the three genes cross-hybridized to a considerable extent. To render this analysis more specific, PCR amplification and hybridization with highly specific **oligonucleotide** probes were used. cDNAs were obtained and amplified by PCR using **oligonucleotide** primers corresponding to **sequences** of exon 3 that were identical for the three MAGE genes discussed herein. The PCR products were then tested for their ability to hybridize to three other **oligonucleotides** that showed complete specificity for one of the three genes (FIG. 12). Control experiments carried out by diluting **RNA** of melanoma MZ2-MEL 3.0 in **RNA** from negative cells indicated that under the conditions used herein the intensity of the signal decreased proportionally to the dilution. . . of one of the three characterized MAGE genes but that of yet another closely related gene that would share the **sequence** of the priming and hybridizing **oligonucleotides**. It can be concluded that the MAGE gene family is expressed by a large **array** of different tumors and that these genes are silent in the normal cells tested to this point.

16. 5,332,666, Jul. 26, 1994, Method, system and reagents for DNA sequencing; James M. Prober, et al., 435/91.5, 6, 968; 436/56, 805; 935/77 [IMAGE AVAILABLE]

US PAT NO: 5,332,666 [IMAGE AVAILABLE] L8: 16 of 78

DETDESC:

DETD(38)

If . . . program proceeds to determine the identity of the peak. The result is the identity of the next base in the **DNA** **sequence**. The program calculates the function W for the current peak as described above, using the **arrays** Rpeak(m) and Tpeak(m) as input data. Each nucleotide base will have associated with it a pair of peaks which give a characteristic W. Thus, based on the value of W for this peak, the program gives as output the **DNA** base identity A, T, C, G. The peak point index m and the **arrays** Rpeak and Tpeak are reset to O, and the program again enters the upper data acquisition loop as shown in. . .

17. 5,324,401, Jun. 28, 1994, Multiplexed fluorescence detector system for capillary electrophoresis; Edward S. Yeung, et al., 204/180.1, 299R; 356/344 [IMAGE AVAILABLE]

US PAT NO: 5,324,401 [IMAGE AVAILABLE] L8: 17 of 78

SUMMARY:

BSUM(10)

There . . . its use for very large numbers (thousands) of capillaries. Because data acquisition is sequential and not truly

parallel, the ultimate **sequencing** speed is generally determined by the observation time needed per **DNA** band for an adequate signal-to-noise ratio. Having more capillaries in the **array** or being able to translate the **array** across the detection region faster will not generally increase the overall **sequencing** speed. To achieve the same signal-to-noise ratio, if the state-of-the-art **sequencing** speed of 100 nucleotides/hour/lane is used, the number of parallel capillaries will have to be reduced proportionately regardless of the scan speed. Moreover, the use of a translational stage can become problematic for a large capillary **array**. Because of the need for translational movement, the amount of cycling and therefore bending of the capillaries naturally increases with the number in the **array**. It has been shown that bending of the capillaries can result in loss in the separation efficiency. This is attributed. . .

DETDESC:

DETD(37)

Crosstalk . . . the fluorescence between neighboring capillaries. Such interferences must be eliminated or reduced to an acceptable level before applications such as **DNA** **sequencing** can be practiced. Crosstalk has two causes: signal light reflections from the walls of adjacent capillaries and scattered light from. . . false peaks. In FIG. 4, the tracings are derived from electropherograms of capillaries No. 6, 9, and 11 of an **array** of thirteen separation capillaries. Peaks A and B are reflections of the fluorescence signal in capillary 9. C and D. . .

DETDESC:

DETD(57)

In this example, **DNA** **sequencing** is done in the same manner as in Example 2. The irradiation of the samples, however, is orthogonal rather than. . . axial. As is shown in FIG. 3, the illuminating ends of the optical fibers are on the side of the **array** of capillaries that is away from the microscope and the camera. Again, the outside diameters the capillaries are 150 microns.. . .

18. 5,316,930, May 31, 1994, Virus resistant plants having antisense RNA; L. Sue Loesch-Fries, et al., 435/172.3, 240.4, 252.3; 536/23.2, 24.5; 800/205, 250 [IMAGE AVAILABLE]

US PAT NO: 5,316,930 [IMAGE AVAILABLE] L8: 18 of 78

SUMMARY:

BSUM(14)

T-**DNA** is often integrated (i.e., inserted) into host **DNA** at multiple sites in the nucleus. Flanking plant **DNA** may be either repeated or low copy number **sequences**. Integrated T-**DNA** can be found in either direct or inverted tandem **arrays** and can be separated by spacers. T-**DNA** can also transform chloroplasts (De Block, M. et al. (1985) EMBO J. 4:1367-1372; see review by Flavell, R. B. (1985). . .

19. 5,312,912, May 17, 1994, Procedures and regulatory DNA sequences for genetically engineering disease resistance and other inducible traits in plants; Lee A. Hadwiger, et al., 536/24.1; 435/320.1; 935/30, 35 [IMAGE AVAILABLE]

US PAT NO: 5,312,912 [IMAGE AVAILABLE] L8: 19 of 78

SUMMARY:

BSUM(13)

The unique **DNA** **sequences** have been identified and analyzed from pea plants which contribute to the pea plant's rapid resistance response to an **array** of plant pathogens including potato pathogens. A method has been described and demonstrated for utilizing the regulatory features of these pea **DNA** **sequences** which include AP-1 sites and topoisomerase consensus sites along with their structural genes, for transforming other dicaryotic plants such as potatoes. Transformed potatoes possessing the **DNA** **sequences** of the regulatory components of pea genes respond intensively to potato pathogen expressing their vitality gene products. Additionally, the pea regulatory **DNA** **sequences** contain A-P-1 binding sites which further increase gene transcription when present with their matching transcription factors. These matching factors can be provided by the co-transformation of **DNA** **sequences** of the animal genes fos and jun, to the recipient dicaryote. This molecular transfer of disease resistance traits provides new. . .

20. 5,308,751, May 3, 1994, Method for sequencing double-stranded DNA; Tihiro Ohkawa, et al., 435/6, 91.2; 436/94 [IMAGE AVAILABLE]

US PAT NO: 5,308,751 [IMAGE AVAILABLE] L8: 20 of 78

SUMMARY:

BSUM(6)

These methods are primarily designed for **sequencing** single-stranded **DNA**, which is produced by denaturing the **DNA** and separating the single strands, or by other methods, such as cloning into single-stranded phage vectors. These **sequencing** methods rely on reactions that produce an **array** of fragments that differ in length by a single base and terminate in an identifiable base. The fragments are resolved. . . such as a radioisotope. Because the resolution of bands on an electrophoretic gel decreases exponentially as the length of the **DNA** fragments increase, these methods only permit **DNA** fragments of up to about 300 to 400 nucleotides to be **sequenced**.

21. 5,306,618, Apr. 26, 1994, Method systems and reagents for DNA sequencing; James M. Prober, et al., 435/6; 356/344; 422/82.07, 82.08; 435/291, 808; 436/171, 172; 935/85 [IMAGE AVAILABLE]

US PAT NO: 5,306,618 [IMAGE AVAILABLE] L8: 21 of 78

DETDESC:

DETD(38)

If . . . program proceeds to determine the identity of the peak. The result is the identity of the next base in the **DNA** **sequence**. The program calculates the function W for the current peak as described above, using the **arrays** Rpeak(m) and Tpeak(m) as input data. Each nucleotide base will have associated with it a pair of peaks which give a characteristic W. Thus, based on the value of W for this peak, the program gives as output the **DNA** base identity A, T, C, G. The peak point index m and the **arrays** Rpeak and Tpeak are reset to 0, and the program again enters the upper data acquisition loop as shown in. . .

22. 5,302,519, Apr. 12, 1994, Method of producing a Mad polypeptide;

Elizabeth M. Blackwood, et al., 435/69.1, 6, 69.3, 70.21, 240.2; 530/350, 351; 536/23.1, 23.5 [IMAGE AVAILABLE]

US PAT NO: 5,302,519 [IMAGE AVAILABLE] L8: 22 of 78

SUMMARY:

BSUM(4)

The . . . molecular mechanism by which Myc mediates its biological effects. The Myc proteins are nuclear phosphoproteins with short half-lives and nonspecific **DNA**-binding activities (2). Functionally important regions exist as both the amino and carboxyl termini of the c-Myc protein (3-5). Indeed, the carboxyl-terminal 85 amino acids of the Myc family proteins share significant **sequence** similarity with two classes of transcription factors, the basic region helix-loop-helix (bHLH) and basic region leucine zipper (bZip) proteins, both. . . bHLH family includes over 60 proteins in vertebrates, yeast, plants, and insects; many, if not all, exhibit nuclear localization, are **sequence**-specific **DNA**-binding proteins, and function as transcriptional regulators(6). The region of **sequence** similarity shared to Myc and other proteins in this class is a critical determinant of function and contains a stretch. . . that the HLH region mediates formation of homo- or heterodimers, which in turn permits the basic regions to form a **DNA** contact surface (9-11). Myc family proteins differ from the bHLH family in that adjacent and carboxyl-terminal to their bHLH motif. . . of leucine residues. This structure is characteristic of the dimerization domains of the bZip family of transcriptional regulators (12). The **array** of nonpolar amino acids forms a hydrophobic face long the amphipathic helic, facilitating specific association of bZip proteins through a parallel coiled-coil interaction (13). Dimerization is critical for **DNA** binding (14, 15).

23. 5,294,323, Mar. 15, 1994, Apparatus for gel electrophoresis; Teruo Togusari, et al., 204/299R, 182.8; 356/344 [IMAGE AVAILABLE]

US PAT NO: 5,294,323 [IMAGE AVAILABLE] L8: 23 of 78

SUMMARY:

BSUM(6)

In . . . and launched horizontally from one side of the plate 74 at a predetermined point on the gel. As the fluorophore-labelled **DNA** fragments migrating through the gel pass through the irradiated region, they will fluoresce successively. The horizontal position of fluorescence emission. . . area in an image intensifier 80. The received signal is amplified and converted to an electric signal in a photodiode **array** 84 for the purpose of various measurements. The results of measurements are processed with a computer so that the **sequences** of the individual **DNA** fragments are calculated to determine the base **sequence** of the **DNA** at issue.

24. 5,286,636, Feb. 15, 1994, DNA cloning vectors with in vivo excisable plasmids; William Huse, et al., 435/172.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,286,636 [IMAGE AVAILABLE] L8: 24 of 78

DETDESC:

DETD(39)

A jumping library is constructed which involves cleavage at the I site to yield fragments, termed I fragments having **sequences** 2:3, 4:5,

etc., at the remote ends of the fragments. The fragments are circularized by ligation under suitable conditions that. . . circularization over multimer formation. It is important to note that circularization occurs at and thereby effects the joining of remote **sequences** 2:3, 4:5, etc. The circular **DNA** molecules are then reacted with one or more enzymes that cleave at the II sites thereby producing an **array** of fragments. Since cleavage does not occur between **sequences** 2:3, 4:5, etc., some of these fragments, termed II fragments, will consist of **DNA** **sequences** (i.e., 2:3, 4:5) that were initially located at opposite ends of the I fragments.

25. 5,273,884, Dec. 28, 1993, Polypetides, antigens or vaccines protective against babesiosis; Kevin G. Gale, et al., 424/191.1, 266.1, 270.1; 435/7.22, 69.1; 530/350, 388.1, 388.6; 536/23.1 [IMAGE AVAILABLE]

US PAT NO: 5,273,884 [IMAGE AVAILABLE] L8: 25 of 78

DETDESC:

DETD(213)

The . . . (approximate length 3100 bp) is composed of a repetitive 5' region (containing approximately 19 copies of a 90 bp repeated **DNA** **sequence** in a head-to-tail tandem **array**) and a unique 3' region 1414 bp in length, which terminates with a row of 13 `A` residues. The unique region **DNA** **sequence** and the derived amino acid **sequence** which terminates with a TGA `stop` condon at position 1285 in the unique region **DNA** **sequence** are shown in FIGS. 17 and 18 respectively.

26. 5,272,254, Dec. 21, 1993, Production of streptavidin-like polypeptides; Harry M. Meade, et al., 530/350, 300, 825 [IMAGE AVAILABLE]

US PAT NO: 5,272,254 [IMAGE AVAILABLE] L8: 26 of 78

DETDESC:

DETD(66)

We . . . plates. We grew the selected cultures as before at 37.degree. C. and printed them out onto nitrocellulose filters in an **array** using a 96-pronged fork. We then hybridized the colonies with the SA-1 probe, prepared as described above, at 30.degree. C.. . . . hybridization methods of Grustein and Hogess, Proc. Natl. Acad. Sci. USA 72, 3961-65 (1975). one of the 2200 colonies contained **DNA** **sequences** which hybridized to the SA-1 probe (colony 62/c).

27. 5,272,071, Dec. 21, 1993, Method for the modification of the expression characteristics of an endogenous gene of a given cell line; Scott C. Chappel, 435/172.3, 69.1, 172.1, 252.3, 320.1; 536/23.1, 24.3; 935/6, 23, 34, 42 [IMAGE AVAILABLE]

US PAT NO: 5,272,071 [IMAGE AVAILABLE] L8: 27 of 78

SUMMARY:

BSUM(4)

It . . . small percentage of the genes present within a given cell type is actually transcribed. The intracellular mechanisms that regulate the **array** of genes to be transcribed are now understood. Cell specific proteins present within the nucleus interact with **DNA** regulatory Segments that are linked with particular genes. This interaction of nuclear proteins with **DNA** regulatory **sequences** is

required for gene transcription. This results in mRNA biosynthesis and ultimate expression of the encoded protein (Mitchell and Tjian,. . .

28. 5,270,163, Dec. 14, 1993, Methods for identifying nucleic acid ligands; Larry Gold, et al., 435/6, 91.2 [IMAGE AVAILABLE]

US PAT NO: 5,270,163 [IMAGE AVAILABLE] L8: 28 of 78

SUMMARY:

BSUM(14)

Joyce and Robertson (Joyce (1989) in **RNA**: Catalysis, Splicing, Evolution, Belfort and Shub (eds.), Elsevier, Amsterdam pp. 83-87; and Robertson and Joyce (1990) Nature 344:467) reported a method for identifying RNAs which specifically cleave single-stranded **DNA**. The selection for catalytic activity was based on the ability of the ribozyme to catalyze the cleavage of a substrate ssRNA or **DNA** at a specific position and transfer the 3'-end of the substrate to the 3'-end of the ribozyme. The product of. . . to the completed product across the junction formed by the catalytic reaction and allowed selective reverse transcription of the ribozyme **sequence**. The selected catalytic **sequences** were amplified by attachment of the promoter of T7 **RNA** polymerase to the 3'-end of the cDNA, followed by transcription to **RNA**. The method was employed to identify from a small number of ribozyme variants the variant that was most reactive for cleavage of a selected substrate. Only a limited **array** of variants was testable, since variation depended upon single nucleotide changes occurring during amplification.

29. 5,268,296, Dec. 7, 1993, DNA vector and recombinant host cell for production of hirullin P6 and P18; Reinhard Maschler, et al., 435/252.3, 69.1, 172.3, 320.1, 942; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,268,296 [IMAGE AVAILABLE] L8: 29 of 78

SUMMARY:

BSUM(49)

The yeast promoter, the optional **DNA** **sequence** coding for the signal peptide, the **DNA** **sequence** coding for the hirullin polypeptide and the **DNA** **sequence** containing yeast transcription termination signals are operably linked to each other, i.e. they are juxtaposed in such a manner that their normal functions are maintained. The **array** is such that the promoter effects proper expression of the hirullin gene (optionally preceded by a signal **sequence**), the transcription termination signals effect proper termination of transcription and polyadenylation and the optional signal **sequence** is linked in the proper reading frame to the hirullin gene in such a manner that the last codon of the signal **sequence** is directly linked to the first codon of the gene coding for the hirullin polypeptide and secretion of the hirullin polypeptide occurs. If the promoter and the signal **sequence** are derived from different genes, the promoter is preferably joined to the signal **sequence** between the major mRNA start and the ATG of the gene naturally linked to the promoter. The signal **sequence** should have its own ATG for translation initiation. The PG,14 junction of these **sequences** may be effected by means of synthetic oligodeoxynucleotide linkers carrying the recognition **sequence** of an endonuclease.

DETDESC:

DETD(123)

Plasmid . . . digestion allows a first site to be digested by HindIII, but the subsequent intercalation of ethidium bromide into the linearised **DNA** interferes with the digestion of the second site, thus enriching for the linearised plasmid **DNA**. The restriction enzyme and ethidium bromide are removed by two consecutive phenol extractions and the **DNA** is ethanol precipitated. This **DNA** is then treated with the **DNA** polymerase large fragment (Klenow enzyme) to fill in the 5' overhangs of the HindIII sites. This end repaired **DNA** is run on an agarose gel to separate the various fragments, including the enriched, end repaired linear. The 3.35 kb pUC18/URA 3 linear **DNA** is cut out of the gel and electro-eluted. This **DNA** is then self ligated with T4 **DNA** ligase, transformed into competent E. coli JM109 cells and plated onto YT plates supplemented with 50 .mu.g/ml ampicillin. Colonies are screened as above to identify plasmid `D`, where the HindIII site at the pUC linker-**array** side of the URAs gene has been end repaired creating a new unique NheI restriction site. Plasmid `D` is digested with the restriction enzyme HindIII to completion and the 5' overhangs are filled in a reaction with Klenow **DNA** polymerase. This **DNA** is then mixed with a large excess of NotI linkers (GCGGCCGC), ligated with T4 **DNA** ligase, transformed into competent E. coli JM109 cells and plated onto TY plates supplemented with 50 .mu.g/ml ampicillin. Colonies are. . . NotI linker added. Plasmid `E` is digested with the restriction enzyme SacI, and the 3' overhangs are repaired with T4 **DNA** polymerase. The **DNA** is then mixed with a large excess of NotI linkers and ligated with T4 **DNA** ligase. This ligation mixture is transformed into competent E. coli JM109 cells and plated onto YT plates supplemented with 50 .mu.g/ml ampicillin. Colonies are screened as above and plasmid pUC18/URA3-N is identified, where the pUC18 **sequences** are now flanked by NotI restriction sites (plasmids `D` and `E` are only intermediates in the construction of pUC18/URA3-N).

30. 5,242,796, Sep. 7, 1993, Method, system and reagents for DNA sequencing; James M. Prober, et al., 435/6; 536/26.7, 26.71, 26.8; 544/243, 244; 549/200, 223 [IMAGE AVAILABLE]

US PAT NO: 5,242,796 [IMAGE AVAILABLE] L8: 30 of 78

DETDESC:

DETD(38)

If . . . program proceeds to determine the identity of the peak. The result is the identity of the next base in the **DNA** **sequence**. The program calculates the function W for the current peak as described above, using the **arrays** Rpeak(m) and Tpeak(m) as input data. Each nucleotide base will have associated with it a pair of peaks which give a characteristic W. Thus, based on the value of W for this peak, the program gives as output the **DNA** base identity A, T, C, G. The peak point index m and the **arrays** Rpeak and Tpeak are reset to 0, and the program again enters the upper data acquisition loop as shown in. . .

31. 5,239,060, Aug. 24, 1993, Muscular dystrophy protein, dystrophin; Louis M. Kunkel, et al., 530/350; 435/69.1 [IMAGE AVAILABLE]

US PAT NO: 5,239,060 [IMAGE AVAILABLE] L8: 31 of 78

SUMMARY:

BSUM(6)

Restriction fragment length polymorphisms (RFLPs) occur when the genomic **DNA** **sequence** in a population of animals varies such that complete digestion with a restriction endonuclease will result in a set of

restriction fragments of one or more different size **arrays**. The differences are due to the presence or absence in the **DNA** **sequence** of sites recognized by the endonuclease; a **sequence** in which the site is present will be cut by the endonuclease giving one **array**, and a **sequence** in which the site is not present will fail to be cut by the endonuclease, giving another **array**.

32. 5,225,584, Jul. 6, 1993, Synthesis of stable water-soluble chemiluminescent 1,2-dioxetanes and intermediates therefor; Edwards Brooks, et al., 558/189; 549/221, 332, 510; 556/405; 558/169, 187 [IMAGE AVAILABLE]

US PAT NO: 5,225,584 [IMAGE AVAILABLE] L8: 32 of 78

DETDESC:

DETD(38)

Such . . . such as phosphatases, esterases, kinases, galactosidases, or the like, and cell surface receptors. These assays can be performed in an **array** of formats, such as solution, both as a two-antibody (sandwich) assay or as a competitive assay, in solid support such. . . in forensic applications using human finger-printing probes, mono and multi loci. The nucleic acid detections can be performed for both **DNA** and **RNA** in a variety of formats, e.g., solution, derivatized tubes or microtiter plates, membranes (dot, slot, Southern and Northern blots) and directly in tissues and cells via in-situ hybridization. **DNA** and **RNA** can also be detected in **sequencing** techniques and histocompatibility assays using chemiluminescent dioxetanes. Such chemiluminescent water-soluble dioxetanes can also be used in biosensors where the ligand-binding. . .

33. 5,221,518, Jun. 22, 1993, DNA sequencing apparatus; Randell L. Mills, 422/62, 67, 82.05; 435/291; 436/89 [IMAGE AVAILABLE]

US PAT NO: 5,221,518 [IMAGE AVAILABLE] L8: 33 of 78

CLAIMS:

CLMS(11)

11. A **DNA** **sequencing** apparatus of claim 1, wherein the analyzing means is an electro-optical ion detector **array** mass spectrometer.

34. 5,215,884, Jun. 1, 1993, Sex-specific DNA probes; Royal A. McGraw, III, 435/6, 172.1, 320.1; 436/27, 501, 811; 935/9, 19, 29, 78, 86, 88 [IMAGE AVAILABLE]

US PAT NO: 5,215,884 [IMAGE AVAILABLE] L8: 34 of 78

SUMMARY:

BSUM(7)

A prominent feature of the human Y chromosome **DNA** is a highly repeated **sequence** not found in females, as described by Bostock, et al, Nature 272,324-328 (1978) and Cooke et al, Chromosoma 87,491-502 (1982). . . . repetitive nature, this material can be visualized directly as a 3.4 kilobase ethidium-staining band by agarose el electrophoresis of male **DNA** after digestion with the restriction enzyme HaeIII. This **sequence** occurs as a tandem **array** of several thousand copies, possibly representing as much as 30% of the human Y chromosome.

35. 5,198,346, Mar. 30, 1993, Generation and selection of novel DNA-binding proteins and polypeptides; Robert C. Ladner, et al., 435/69.1, 172.3, 252.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,198,346 [IMAGE AVAILABLE] L8: 35 of 78

DETDESC:

DETD(231)

Landschulz et al. (LAND88) have identified a new class of eukaryotic **DNA**-binding proteins that includes C/EBP, c-Myc, Fos, Jun, and GCN4. The **sequences** of members of the class contain a periodic repetition of leucine residues such that, according to the authors' model, alpha helix formation results in an **array** of leucines down one side of the helix. Interaction of this **array** with such an **array** on another protein molecule forms a "leucine zipper" (LAND88) which, though not directly implicated in the binding of these proteins to **DNA**, may influence the ability of these proteins to bind **DNA** by changing protein structure through protein-protein interactions. Landschulz et al. suggest that heterologous aggregates may form by association of two. . .

36. 5,196,328, Mar. 23, 1993, Modified cloning vectors for restriction mapping, their preparation and use; Kenneth D. Tartof, 435/172.3, 5, 6, 29, 320.1; 536/24.2; 935/26, 29, 31, 78 [IMAGE AVAILABLE]

US PAT NO: 5,196,328 [IMAGE AVAILABLE] L8: 36 of 78

SUMMARY:

BSUM(6)

One commonly used procedure for obtaining a restriction map is by digesting the **DNA** molecule of interest, or target **DNA**, with combinations of restriction enzymes. In order to simplify the procedure, a primary digestion is preferably carried out to limit the number of fragments produced. The primary digest is produced using an enzyme having an infrequent recognition **sequence**, such as enzymes that recognize hexanucleotide **sequences**. As is known, the primary **DNA** fragments may be isolated and recovered following separation, e.g. by electrophoresis. A **DNA** fragment obtained in the primary digest may be cleaved with additional restriction enzymes, and compared on a gel with appropriate. . . of known size. From the data obtained, it is possible to postulate a restriction map which accounts for the observed **array** of fragments. In building up a restriction map by this procedure, one attempts to assign cleavage sites by trial and. . .

SUMMARY:

BSUM(7)

Resolution of the restriction map obtained by the above-described method of digesting a **DNA** **sequence** with a succession of restriction enzymes may be enhanced if the digestion is carried out with different restriction enzymes, both singly and together. By producing fragments from both single and double digestions, a greater **array** of fragments is generated for use in formulating a restriction map. Similarly, additional specificity concerning the restriction sites in a **DNA** molecule may be obtained by performing both complete and partial digestions with one or more restriction enzymes.

SUMMARY:

BSUM(17)

In . . . herein as the recession hybridization detection (RHD) technique, after the first digestion of the above-described method is completed, the resulting **DNA** pieces are reacted with an exonuclease enzyme to recess the 3' ends. Recession occurs at the end of the **DNA** pieces containing the infrequent cutter linker construct which, as a result of the first digestion, is present at only one end of each **DNA** piece. To the exposed single-stranded end of each fragment created by exonuclease action is hybridized a labeled, synthetic **oligonucleotide** complementary to the exposed single-stranded **DNA** **sequence**. The labeled fragments are then further digested with the second restriction enzyme, separated, e.g. by gel electrophoresis, and exposed to X-ray film. The resulting autoradiographic pattern displays an **array** of fragments which are ordered from the labeled terminus, from which the location of restriction sites within the **DNA** molecule of interest is determinable.

37. 5,187,084, Feb. 16, 1993, Automatic air temperature cycler and method of use in polymerose chain reaction; G. Anders Hallsby, 435/91.2, 91.21, 287, 290, 316; 935/77, 78, 85, 88 [IMAGE AVAILABLE]

US PAT NO: 5,187,084 [IMAGE AVAILABLE] L8: 37 of 78

ABSTRACT:
Apparatus and method for automatically developing, maintaining and repetitively duplicating a selectable predetermined temperature profile for replicating and amplifying a **sequence** of a stretch of **DNA** or **RNA** through use of a polymerase. An **array** of sample-containing vessels is supported in a reaction chamber through which a heat transfer medium in heat-exchange relationship with the vessels. The temperature of the air is controlled as a function of time to provide a preselectable **sequence** defining a temperature profile. The profile is cyclically repetitively reproduced to effect amplification of the desired **sequence** of **DNA** or **RNA**.

SUMMARY:

BSUM(9)

The . . . a method for automatically developing and maintaining, and repetitively duplicating a selectable predetermined temperature profile for replicating and amplifying a **sequence** of a stretch of **DNA** through a polymerase catalyzed reaction. An **array** of sample-containing vessels is supported in a reaction chamber through which air at controlled temperatures is forcibly circulated as a. . . relationship with the vessels. The temperature of the air is controlled as a function of time to provide a preselectable **sequence** defining a temperature profile. The profile is cyclically repetitively reproduced to effect replication of and amplification of the desired **sequence** of the **DNA**.

38. 5,185,440, Feb. 9, 1993, cDNA clone coding for Venezuelan equine encephalitis virus and attenuating mutations thereof; Nancy L. Davis, et al., 536/23.72; 435/235.1, 236, 320.1; 935/10, 65 [IMAGE AVAILABLE]

US PAT NO: 5,185,440 [IMAGE AVAILABLE] L8: 38 of 78

SUMMARY:

BSUM(2)

Venezuelan . . . encephalitis virus (VEE) is a member of the alphavirus genus of the Togaviridae. The viral genome is a

single-stranded, messenger-sense **RNA**, modified at the 5'-end with a methylated cap, and at the 3'-end with a variable-length poly (A) tract. Structural subunits containing a single viral protein, C, associate with the **RNA** genome in an icosahedral nucleocapsid. In the virion, the capsid is surrounded by a lipid envelope covered with a regular **array** of transmembranal protein spikes, each of which consists of a heterodimeric complex of two glycoproteins, E1 and E2 (Pedersen and. . . alphaviruses, Sindbis virus and Semliki Forest virus (reviewed in Schlesinger and Schlesinger, 1986). For example, details of the partial genome **sequence** (Kinney et al., 1986) demonstrate that VEE structural proteins are translated in the form of a polyprotein from a 26S. . . Ruohonen, 1983; Strauss et al., 1984; Hardy and Strauss, 1988). The mature nonstructural proteins are required or replication of genome **RNA** and the synthesis of 26S subgenomic mRNA.

39. 5,182,200, Jan. 26, 1993, T-DNA promoters; Jerry L. Slightom, et al., 435/172.3, 69.1, 70.1, 240.4, 252.2, 252.3, 252.33; 536/23.2, 23.6, 24.1; 935/35, 36, 41, 67 [IMAGE AVAILABLE]

US PAT NO: 5,182,200 [IMAGE AVAILABLE] L8: 39 of 78

SUMMARY:

BSUM(33)

A portion of the Ti or Ri plasmid is found in the **DNA** of tumorous plant cells. T-**DNA** may be integrated (i.e. inserted) into host **DNA** at multiple sites in the nucleus. Flanking plant **DNA** may be either repeated or low copy number **sequences**. Integrated T-**DNA** can be found in either direct or inverted tandem **arrays** and can be separated by spacers. Much non-T-**DNA** Ti plasmid **DNA** appears to be transferred into the plant cell prior to T-**DNA** integration (H. Joos et al. (1983) EMBO J. 2:2151-2160). T-**DNA** has direct repeats of about 25 base pairs associated with the borders, i.e. with the T-**DNA**/plant **DNA** junctions, which may be involved in either transfer from Agrobacterium or integration into the host genome.

40. 5,180,667, Jan. 19, 1993, Genes encoding eglin C mutants; Markus G. Grutter, et al., 435/69.2, 240.1, 254.2, 320.1; 536/23.5 [IMAGE AVAILABLE]

US PAT NO: 5,180,667 [IMAGE AVAILABLE] L8: 40 of 78

DETDESC:

DETD(68)

An . . . in yeast requires a strong yeast promoter, preferably an inducible promoter, and a yeast transcription termination signal in a tandem **array** separated by unique restriction sites for the insertion of foreign genes. An expression vector also contains yeast **DNA** **sequences** that allow autonomous replication in yeast and lead to a high plasmid copy number. These **sequences** preferably are yeast 2 .mu. **sequences**. The vector also has a yeast selectable marker, preferably the yeast LEU2 gene, as well as pBR322 **DNA** **sequences** with the origin of replication and the ampicillin resistance gene for amplification in E. coli. Such a vector is a. . .

41. 5,179,017, Jan. 12, 1993, Processes for inserting DNA into eucaryotic cells and for producing proteinaceous materials; Richard Axel, et al., 435/240.2, 69.1, 70.3; 935/34, 70 [IMAGE AVAILABLE]

US PAT NO: 5,179,017 [IMAGE AVAILABLE] L8: 41 of 78

DETDESC:

DETD(48)

Cleavage of **DNA** from .PHI.X transformants with Eco RI generates a series of fragments which contain .PHI.X **DNA** **sequences**. These fragments may reflect multiple integration events. Alternatively, these fragments could result from tandem **arrays** of complete or partial .PHI.X **sequences** which are not integrated into cellular **DNA**. To distinguish between these possibilities, transformed cell **DNA** was cut with BAM HI or Eco RI, neither of which cleaves the .PHI.X genome. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. Identical patterns would be generated from undigested **DNA** and from **DNA** cleaved with either of these enzymes. If the **sequences** are integrated, then BAM HI and Eco RI should recognize different sites in the flanking cellular **DNA** and generate unique restriction patterns. **DNA** from clones .PHI.X4 and .PHI.X5 was cleaved with BAM III or Eco RI and analyzed by Southern hybridization. In each. . . pattern with Eco RI fragments differed from that observed with the BAM HI fragments. Furthermore, the profile obtained with undigested **DNA** reveals annealing only in very high molecular weight regions with no discrete fragments observed. Similar observations were made on clone .PHI.X1. Thus, the most of the .PHI.X **sequences** in these three clones are integrated into cellular **DNA**.

42. 5,173,410, Dec. 22, 1992, Transfer vector; Paul G. Ahlquist, 435/91.3, 69.1, 172.3, 235.1, 317.1; 935/4, 17, 18, 21, 41 [IMAGE AVAILABLE]

US PAT NO: 5,173,410 [IMAGE AVAILABLE] L8: 42 of 78

DETDESC:

DETD(12)

The vector used in the present invention for the insertion, propagation and manipulation of the BamHI-ClaI **DNA** fragment from the expression vector pCQV2 (FIG. 1) was M13mp9 (Messing, J. and Vieira, J. (1982) Gene 19:269-276). The M13mp9. . . (e.g., f1 or fd). Other filamentous, single stranded phages could equally well be utilized in these experiments (The Single Stranded **DNA** phages (1978), Denhardt et al. (eds.) Cold Spring Harbor Laboratory, New York). M13mp9 was derived from another M13 engineered phage, i.e., M13mp7. The cloning of **DNA** into the replicative form (RF) of M13 has been facilitated by a series of improvements which produced the M13mp7 cloning vehicle (Gronenborn, B. and J. Messing (1978) Nature, Lond. 272:375-377; Messing, J. (1979) Recombinant **DNA** Technical Bulletin, NIH Publication No. 79- 99, 2, No. 2 43-48; Messing, J. et al. (1981) Nucl. Acids Res. 9:309-321).. . . a medium containing IPTG and X-gal (Malamy, M. H. et al. (1972) Mol. Gen. Genet. 119:207ff). In addition, a small **DNA** fragment synthesized in vitro and containing an **array** of restriction cleavage sites [a multiple cloning site (MCS)] was inserted into the structural region of the .beta.-galactosidase gene fragment. In spite of these insertions the M13mp7 **DNA** is still infective and the modified lac **DNA** is able to encode the synthesis of a functional .beta.-galactosidase .alpha.-peptide (Langley, K. E. et al. (1975) Proc. Nat:. Acad. Sci. U.S.A. 72:1254-1257). This synthesized **DNA** fragment in M13mp7 contains two sites each for the EcoRI, BamHI, SalI, AccI and HincII restriction enzymes arranged symmetrically with. . . viral (+) strand. This depends on the fragment orientation elative to the M13 genome after ligation. The insertion of a **DNA** fragment into one of these

restriction sites is readily monitored because the insertion results in a non-functional .alpha.-peptide and the. . . in blue plaques; a non-functional .alpha.-peptide results in colorless plaques (Messing, J. and B. Bronenborn (1978) In The Single Stranded **DNA** Phages, Denhardt et al. (eds.), Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., pp. 449-453). M13mp7 has found wide application in the dideoxy nucleotide **sequencing** procedure (Sanger, F. et al. (1977) Proc. Nat. Acad. Sci. U.S.A. 74:5463-5467).

43. 5,168,049, Dec. 1, 1992, Production of streptavidin-like polypeptides; Harry M. Meade, et al., 435/69.1, 69.7, 69.8, 172.3, 240.1, 240.2, 240.4, 252.3, 252.33, 252.35, 254.11, 254.2, 320.1; 935/10, 11 [IMAGE AVAILABLE]

US PAT NO: 5,168,049 [IMAGE AVAILABLE] L8: 43 of 78

DETDESC:

DETD(64)

We . . . plates. We grew the selected cultures as before at 37.degree. C. and printed them out onto nitrocellulose filters in an **array** using a 96- pronged fork. We then hybridized the colonies with the SA-1 probe, prepared as described above, at 30.degree.. . . hybridization methods of Grunstein and Hogness, Proc. Natl. Acad. Sci. USA 72, 2961-65 (1975). One of the 2200 colonies contained **DNA** **sequences** which hybridized to the SA-1 probe (colony 62/c).

44. 5,166,315, Nov. 24, 1992, Sequence-specific binding polymers for duplex nucleic acids; James E. Summerton, et al., 528/406, 403, 422, 423, 425 [IMAGE AVAILABLE]

US PAT NO: 5,166,315 [IMAGE AVAILABLE] L8: 44 of 78

CLAIMS:

CLMS(1)

It is claimed:

1. A polymer composition effective to bind in a **sequence**-specific manner to a target **sequence** of a duplex **polynucleotide** containing different Watson-Crick basepair orientations at selected target **sequence** positions, comprising a selected **sequence** of subunits having the form: ##STR8## where Y is a 2- or 3-atom length, uncharged subunit linkage group; R is. . .
G:C orientation, R.sub.i is selected from the group consisting of planar bases having the following ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR9## where the * ring position may carry a hydrogen-bond acceptor group; and (d). . . A:T orientation, R.sub.i is selected from the group consisting of planar bases having the following ring structures and hydrogen bonding **arrays**, where B indicates the polymer backbone: ##STR10## where the * ring position may carry a hydrogen-bond donating group.

45. 5,166,100, Nov. 24, 1992, Methods of making nanometer period optical gratings; Arthur C. Gossard, et al., 437/228, 128, 245 [IMAGE AVAILABLE]

US PAT NO: 5,166,100 [IMAGE AVAILABLE] L8: 45 of 78

DETDESC:

DETD(11)

The . . . deposited on the ultragrating would be preferentially absorbed in the grooves and the molecules would then present an ordered, aligned **array** for convenience in analysis, for the enhancement of chemical reactivity of the molecules, for use in the formation of catalytic structures, and in the case of **DNA**, for convenience in **sequencing**.

46. 5,162,654, Nov. 10, 1992, Detection apparatus for electrophoretic gels; Anthony J. Kostichka, et al., 250/458.1; 204/182.8, 299R; 250/302, 461.2; 356/344 [IMAGE AVAILABLE]

US PAT NO: 5,162,654 [IMAGE AVAILABLE] L8: 46 of 78

SUMMARY:

BSUM(4)

The revolution in modern biology in the past decades has been driven in large part by the development of an **array** of new methods and tools for the manipulation of molecules of **DNA**, the basic substance of molecular genetics. Included within the **array** of those tools has been the ability to determine the precise chemical structure of large **DNA** molecules. **DNA** molecules are linear chains in which the links in the chain are made up of a series of one of. . . chemical sub-units, referred to as nucleotides or bases, chemically fastened to a common backbone. Thus the structure of a large **DNA** molecule is determined by the **sequence** of the bases along the very long continuous **DNA** molecule. The ability to **sequence** **DNA** molecules is, in essence, the ability to read the genetic code and determine the structure of individual **DNA** molecules, which code for specific genes or traits.

47. 5,149,636, Sep. 22, 1992, Method for introducing cloned, amplifiable genes into eucaryotic cells and for producing proteinaceous products; Richard Axel, et al., 435/69.1, 6, 69.2, 69.3, 69.4, 69.51, 69.6, 91.1, 91.32, 172.3, 191, 193, 194, 240.2, 240.4, 320.1, 811, 948; 514/2, 3, 4, 23; 935/4, 27, 31, 42, 56, 58, 66 [IMAGE AVAILABLE]

US PAT NO: 5,149,636 [IMAGE AVAILABLE] L8: 47 of 78

DETDESC:

DETD(57)

In considering possible mechanisms responsible for the correction process, it is important to discern whether the **sequence** changes observed are restricted to a localized region about the aprt gene or whether gross reorganization extends throughout the amplified **array**. The physical changes in the amplification unit upon correction of cell lines constructed solely with defined plasmids were therefore examined. As described above, these cloned cell lines maintain a transforming element which consists of plasmid **sequences** for which cloned probes are available. In this way, a mapped amplified **array** can be analyzed before and after correction has occurred. Three aprt.sup.+ tk.sup.- lines containing derivatives of the plasmid pBR322 were. . . in each of these lines, the aprt gene remained linked to the tk gene and significant lengths of the transforming **DNA** have been amplified 20 to 40 fold. Of these 14 lines, 12 produced aprt.sup.- tk.sup.+ mutants at detectable frequencies. It. . .

DETDESC:

DETD(59)

pBR322 **sequences** were utilized as a probe to examine the

organization of the flanking **DNA** in the amplification unit. Examination indicates that the amplification unit remains essentially unchanged upon correction. Each mutant retains the unique **array** of plasmid **sequences** displayed by its aprt.sup.+ parent. Two bands amplified in the parent are absent in the aprt.sup.- mutants. Hybridization with aprt. . . the aprt gene deleted in the aprt.sup.- mutants. The second band may reflect one breakpoint of the deletion in flanking **DNA**. Thus, the correction process seems to be highly conservative. Rearrangements are restricted to a unique change about the aprt gene which appears identical in all units of the amplified **array**.

DETDESC:

DETD(82)

One final mechanism for correction which must be considered involves genetic recombination. In eucaryotes, individual repeat units in a tandem **array** frequently show striking homogeneity. Maintenance of **sequence** homogeneity is thought to arise either by unequal crossing-over events or gene conversion [Smith, G. P. (1976). Science 191, 528-535;. . . and Petes, J. D. (1981). Nature 289, 144-148]. Direct estimates of the frequency of unequal sister strand exchange among repeated **DNA** **sequences** in mitotic yeast cells suggest this mechanism can maintain the observed homogeneity [Szostak, J. W. and Wu, R. (1980). Nature. . . explanation for the fixation of the mutant aprt gene for two reasons. First, unequal crossing-over between the highly repeated pBR **sequences** in these cell lines would scramble their relationship to one another, resulting in an altered Southern blot banding pattern, which. . . Computer simulations of the unequal crossing-over process has indicated that the probability of fixation of a mutant allele in an **array** of 30 wild-type genes in such a few generations less than 10.sup.-8, assuming one sister chromatid exchange per generation.

48. 5,128,256, Jul. 7, 1992, DNA cloning vectors with in vivo excisable plasmids; William Huse, et al., 435/172.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,128,256 [IMAGE AVAILABLE] L8: 48 of 78

DETDESC:

DETD(40)

A jumping library is constructed which involves cleavage at the I site to yield fragments, termed I fragments having **sequences** 2:3, 4:5, etc., at the remote ends of the fragments. The fragments are circularized by ligation under suitable conditions that. . . circularization over multimer formation. It is important to note that circularization occurs at and thereby effects the joining of remote **sequences** 2:3, 4:5, etc. The circular **DNA** molecules are then reacted with one or more enzymes that cleave at the II sites thereby producing an **array** of fragments. Since cleavage does not occur between **sequences** 2:3, 4:5, etc., some of these fragments, termed II fragments, will consist of **DNA** **sequences** (i.e., 2:3, 4:5) that were initially located at opposite ends of the I fragments.

49. 5,122,448, Jun. 16, 1992, Assay of anti-Epstein-Barr virus nuclear antigen antibodies with synthetic polypeptides; John H. Vaughan, et al., 435/5, 7.1, 7.9, 7.92, 7.93, 7.94, 974; 436/518, 531, 536, 540, 811, 812, 823; 530/326, 327, 810; 930/DIG.800 [IMAGE AVAILABLE]

US PAT NO: 5,122,448 [IMAGE AVAILABLE] L8: 49 of 78

SUMMARY:

BSUM(32)

The correct reading frame of a **DNA** **sequence** coding for a protein, and therefore the protein's amino acid residue **sequence**, may be determined through the use of antibodies. This strategy involves manufacturing an **array** of protein fragments or polypeptides whose amino acid residue **sequences** correspond to the **sequences** obtained from the three possible gene products. The protein fragments or polypeptides that induce antibodies that immunoreact with the gene's. . .

50. 5,116,725, May 26, 1992, Assay for Epstein-Barr virus infection with solid phase bound synthetic polypeptides; John H. Vaughan, et al., 435/5, 7.9, 7.94, 21, 25, 28, 174, 974, 975; 436/518, 536, 540, 541, 811, 812, 823; 530/326, 327, 806, 810; 930/DIG.800 [IMAGE AVAILABLE]

US PAT NO: 5,116,725 [IMAGE AVAILABLE] L8: 50 of 78

SUMMARY:

BSUM(31)

The correct reading frame of a **DNA** **sequence** coding for a protein, and therefore the protein's amino acid residue **sequence**, may be determined through the use of antibodies. This strategy involves manufacturing an **array** of protein fragments or polypeptides whose amino acid residue **sequences** correspond to the **sequences** obtained from the three possible gene products. The protein fragments or polypeptides that induce antibodies that immunoreact with the gene's. . .

51. 5,114,922, May 19, 1992, Polypeptides with an anticoagulant activity; Reinhard Maschler, et al., 514/12; 530/324 [IMAGE AVAILABLE]

US PAT NO: 5,114,922 [IMAGE AVAILABLE] L8: 51 of 78

SUMMARY:

BSUM(49)

The yeast promoter, the optional **DNA** **sequence** coding for the signal peptide, the **DNA** **sequence** coding for the hirullin polypeptide and the **DNA** **sequence** containing yeast transcription termination signals are operably linked to each other, i.e. they are juxtaposed in such a manner that their normal functions are maintained. The **array** is such that the promoter effects proper expression of the hirullin gene (optionally preceded by a signal **sequence**), the transcription termination signals effect proper termination of transcription and polyadenylation and the optional signal **sequence** is linked in the proper reading frame to the hirullin gene in such a manner that the last codon of the signal **sequence** is directly linked to the first codon of the gene coding for the hirullin polypeptide and secretion of the hirullin polypeptide occurs. If the promoter and the signal **sequence** are derived from different genes, the promoter is preferably joined to the signal **sequence** between the major mRNA start and the ATG of the gene naturally linked to the promoter. The signal **sequence** should have its own ATG for translation initiation. The junction of these **sequences** may be effected by means of synthetic oligodeoxynucleotide linkers carrying the recognition **sequence** of an endonuclease.

DETDESC:

DETD(122)

Plasmid . . . digestion allows a first site to be digested by HindIII, but the subsequent intercalation of ethidium bromide into the linearised **DNA** interferes with the digestion of the second site, thus enriching for the linearised plasmid **DNA**. The restriction enzyme and ethidium bromide are removed by two consecutive phenol extractions and the **DNA** is ethanol precipitated. This **DNA** is then treated with the **DNA** polymerase large fragment (Klenow enzyme) to fill in the 5' overhangs of the HindIII sites. This end repaired **DNA** is run on an agarose gel to separate the various fragments, including the enriched, end repaired linear. The 3.35 kb pUC18/URA3 linear **DNA** is cut out of the gel and electro-eluted. This **DNA** is then self ligated with T4 **DNA** ligase, transformed into competent E. coli JM109 cells and plated onto YT plates supplemented with 50 .mu.g/ml ampicillin. Colonies are screened as above to identify plasmid `D`, where the HindIII site at the pUC linker-**array** side of the URA3 gene has been end repaired creating a new unique NheI restriction site. Plasmid `D` is digested with the restriction enzyme HindIII to completion and the 5' overhangs are filled in a reaction with Klenow **DNA** polymerase. This **DNA** is then mixed with a large excess of NotI linkers (GCGGCCGC), ligated with T4 **DNA** ligase, transformed into competent E. coli JM109 cells and plated onto TY plates supplemented with 50 .mu.g/ml ampicillin. Colonies are. . . NotI linker added. Plasmid `E` is digested with the restriction enzyme SacI, and the 3' overhangs are repaired with T4 **DNA** polymerase. The **DNA** is then mixed with a large excess of NotI linkers and ligated with T4 **DNA** ligase. This ligation mixture is transformed into competent E. coli JM109 cells and plated onto YT plates supplemented with 50 .mu.g/ml ampicillin. Colonies are screened as above and plasmid pUC18/URA3-N is identified, where the pUC18 **sequences** are now flanked by NotI restriction sites (plasmids `D` and `E` are only intermediates in the construction of pUC18/URA3-N).

52. 5,114,840, May 19, 1992, Method for determining the nucleotide sequence of a novel .alpha.5(IV) chain of human type IV collagen; Karl Tryggvason, et al., 435/6, 91.41, 91.5, 172.3, 240.1, 252.3, 252.33, 259, 320.1; 536/23.5; 935/9, 23, 24, 29, 31, 55, 56, 58, 73 [IMAGE AVAILABLE]

US PAT NO: 5,114,840 [IMAGE AVAILABLE] L8: 52 of 78

DETDESC:

DETD(2)

Proteins . . . of amino acids that are bound to each other in chain like structures (polypeptide chains). Depending on the amino acid **sequence**, the proteins can fold in a variety of ways, each protein having a distinct amino acid **sequence**, form, and function. The amino acid **sequence** is predetermined in the information contained in the **DNA** **sequence** of the corresponding gene. This **DNA** **sequence**, in turn, consists of a linear **array** of four bases, adenine (A), guanine (G), thymine (T), and cytosine (C). Mutations, i.e. changes in the **DNA** **sequence** of a gene, can, therefore, directly cause changes in the structure and consequently the function of the protein. Such an. . .

53. 5,112,735, May 12, 1992, Detection of lymphocyte amplification; Richard J. Albertini, 435/6, 7.1, 240.1, 240.2; 436/63, 94, 501, 506; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 5,112,735 [IMAGE AVAILABLE] L8: 53 of 78

DETDESC:

DETD(2)

In . . . is evidenced by the commonality of their specific antigen receptors, antibodies in B-cells and TCRs in T-cells. The amino acid **sequence** of a TCR peptide, for example, renders it specific to a particular and limited **array** of antigens. In any individual there are a vast variety of TCR types estimated at 10.sup.6 to 10.sup.7. The variety. . . of TCR. While not wishing to be bound by this explanation, it is believed that translocations or rearrangements of the **DNA** of the V, C, D and J regions is the mechanism by which a T-lymphocyte is committed to expressing a. . .

54. RE 33,897, Apr. 21, 1992, Synthetic polypeptides and antibodies related to Epstein-Barr virus nuclear antigen; John H. Vaughan, et al., 530/326; 424/186.1; 514/8, 13, 14, 15, 21; 530/327, 328, 350, 351, 387.9, 389.4, 395, 826 [IMAGE AVAILABLE]

US PAT NO: RE 33,897 [IMAGE AVAILABLE] L8: 54 of 78

SUMMARY:

BSUM(19)

The correct reading frame of a **DNA** **sequence** coding for a protein, and therefore the protein's amino acid residue **sequence**, may be determined through the use of antibodies. This strategy involves manufacturing an **array** of protein fragments or polypeptides whose amino acid residue **sequences** correspond to the **sequences** obtained from the three possible gene products. The protein fragments or polypeptides that induce antibodies that immunoreact with the gene's. . .

55. 5,102,796, Apr. 7, 1992, Plant structural gene expression; Timothy C. Hall, et al., 435/172.3, 252.2, 252.3, 320.1; 536/23.2, 23.6, 23.7, 24.1; 935/11, 18, 30, 35, 67 [IMAGE AVAILABLE]

US PAT NO: 5,102,796 [IMAGE AVAILABLE] L8: 55 of 78

SUMMARY:

BSUM(30)

In contrast to the situation in octopine-type tumors, nopaline T-**DNA** is integrated into the host genome in one continuous fragment (M. Lemmers et al. (1980) J. Mol. Biol. 144:353-376, P. Zambryski et al. (1980) Science 209:1385 1391). Direct tandem repeats were observed. T-**DNA** of plants regenerated from teratomas had minor modifications in the border fragments of the inserted **DNA** (Lemmers et al. supra). **Sequence** analysis of the junction between the right and left borders revealed a number of direct repeats and one inverted repeat.. . . nucleotide (P. Zambryski et al. (1982) J. Molec. Appl. Genet. 1 361-370). Left and right borders in junctions of tandem **arrays** where separated by spacers which could be over 130 bp. The spacers were of unknown origin and contained some T-**DNA** **sequences**. T-**DNA** was found to be integrated into both repeated and low copy number host **sequences**.

56. 5,102,785, Apr. 7, 1992, Method of gene mapping; Kenneth J. Livak, et al., 435/6, 91.53; 436/94, 501; 935/77 [IMAGE AVAILABLE]

US PAT NO: 5,102,785 [IMAGE AVAILABLE] L8: 56 of 78

SUMMARY:

BSUM(5)

Restriction enzymes provide a tool to rapidly analyze **DNA** segments to obtain a limited amount of **sequence** information. Each restriction enzyme recognizes a specific **sequence** of **DNA**, normally four to eight nucleotide pairs in length, and cleaves **DNA** at or near this recognition **sequence**. Digestion of a **DNA** segment with a particular restriction enzyme thus generates a characteristic **array** of fragments. Typically, these fragments are separated according to length by electrophoresis through an appropriate gel matrix. The sizes of the fragments are dependent on the exact **sequence** recognized by the restriction enzyme and the spatial distribution of the recognition **sequence** within the **DNA** segment. Thus, cleavage of a **DNA** segment with a restriction enzyme indicates that a particular short recognition **sequence** is present; the number of fragments produced indicates how many times the recognition **sequence** occurs; and the sizes of the fragments indicate the distance, in nucleotides, between adjacent recognition sites.

57. 5,100,661, Mar. 31, 1992, Method for regulating cellular signal transducing system; Geoffrey J. Schmidt, 424/146.1, 152.1, 450, 812; 435/240.2, 244; 530/388.26 [IMAGE AVAILABLE]

US PAT NO: 5,100,661 [IMAGE AVAILABLE] L8: 57 of 78

DETDESC:

DETD(7)

A-protein, . . . genetically engineered to express A-protein, or a portion or analog thereof. This may be accomplished by now well established recombinant **DNA** technologies known to those skilled in the art. The recombinant procedure may include the isolation or synthesis of a gene. . . encoding an A-protein, a portion, or analog thereof, and the integration of that gene into a plasmid. The amino acid **sequence** of A-protein may be established readily given this disclosure. Gene synthesis from synthetic **oligonucleotides** and known mutagenesis techniques provide the technologies to prepare an **array** of analogs, truncated A-protein forms, and fused proteins comprising A-protein or a domain thereof. Production of such materials further may include the transformation of an appropriate host cell with a vector harboring the recombinant **DNA**, culturing that transformed host cell, and isolation of the expressed protein. Given the availability of A-protein rich samples producible as. . .

58. 5,096,815, Mar. 17, 1992, Generation and selection of novel DNA-binding proteins and polypeptides; Robert C. Ladner, et al., 435/69.1, 172.3, 252.3, 320.1 [IMAGE AVAILABLE]

US PAT NO: 5,096,815 [IMAGE AVAILABLE] L8: 58 of 78

DETDESC:

DETD(207)

Landschulz et al. (LAND88) have identified a new class of eukaryotic **DNA**-binding proteins that includes C/EBP, c-Myc, Fos, Jun, and GCN4. The **sequences** of members of the class contain a periodic repetition of leucine residues such that, according to the authors' model, alpha helix formation results in an **array** of leucines down one side of the helix. Interaction of this **array** with such an **array** on another protein molecule forms a "leucine zipper" (LAND88) which, though not directly implicated in the binding of these proteins to **DNA**, may influence the ability of these proteins to bind **DNA** by changing protein structure through protein-protein interactions. Landschulz et al.

suggest that heterologous aggregates may form by association of two. . .

59. 5,079,229, Jan. 7, 1992, Modified eglin proteins; Markus G. Grutter, et al., 514/12; 435/69.2; 530/324, 855 [IMAGE AVAILABLE]

US PAT NO: 5,079,229 [IMAGE AVAILABLE] L8: 59 of 78

DETDESC:

DETD(69)

An . . . in yeast requires a strong yeast promoter, preferably an inducible promoter, and a yeast transcription termination signal in a tandem **array** separated by unique restriction sites for the insertion of foreign genes. An expression vector also contains yeast **DNA** **sequences** that allow autonomous replication in yeast and lead to a high plasmid copy number. These **sequences** preferably are yeast 2.mu. **sequences**. The vector also has a yeast selectable marker, preferably the yeast LEU2 gene, as well as pBR322 **DNA** **sequences** with the origin of replication and the ampicillin resistance gene for amplification in E. coli. Such a vector is a. . .

60. 4,973,845, Nov. 27, 1990, Very high resolution autofluoroscope for ionizing radiation; Roland Mastrippolito, et al., 250/368, 366, 367 [IMAGE AVAILABLE]

US PAT NO: 4,973,845 [IMAGE AVAILABLE] L8: 60 of 78

DETDESC:

DETD(28)

In . . . denoted B in FIG. 2a, as previously mentioned. The radioelements migrate into the gel and pass in front of the **array** R of the autofluoroscope in accordance with the invention. The simultaneous recording of the detection time and the position of. . . the emitted electrons gives the radioelement migration speed spectrum and this spectrum can be computer processed to deduce the corresponding **DNA** **sequence**. The radioelements are caused to migrate by the electric field applied to the electrophoresis gel in the conventional way.

61. 4,970,672, Nov. 13, 1990, Data processing system, and keypad assembly for inputting data in such system; Hiram R. Snodgrass, 364/709.12; 33/1M [IMAGE AVAILABLE]

US PAT NO: 4,970,672 [IMAGE AVAILABLE] L8: 61 of 78

ABSTRACT:
A data entry keypad assembly, comprising a keypad including an **array** of keys, and a positioning locator secured to the keypad to form a unitary keypad assembly therewith, whereby the keypad. . . The keypad assembly, computer software, and data processing system of the invention have particular utility to the inputting of primary **DNA** nucleotide **sequence** data from autoradiograms into a digital computer for storage and retrieval, and/or processing thereof.

DETDESC:

DETD(30)

In application to molecular biology applications involving entry of nucleotide **sequences** of **DNA** molecules, the top row of keys 152,

154, 156, and 158 of the 12-key **array** illustratively shown in the embodiment of FIGS. 1 and 2, can be configured as nucleoside symbols (A, C, G, and. . . window are employed to maintain the proper position of the keypad assembly 110 in the nucleotide field, or printed base **sequence**, during data entry.

62. 4,956,288, Sep. 11, 1990, Method for producing cells containing stably integrated foreign DNA at a high copy number, the cells produced by this method, and the use of these cells to produce the polypeptides coded for by the foreign DNA; James G. Barsoum, 435/172.3, 69.1, 70.1, 71.1, 172.1, 252.3; 935/16, 33, 52 [IMAGE AVAILABLE]

US PAT NO: 4,956,288 [IMAGE AVAILABLE] L8: 62 of 78

DETDESC:

DETD(53)

In cells containing high copy number **DNA**, produced by traditional gene amplification techniques, the individual repeating units are usually very large, and may range in size from hundreds to thousands of kilobase pairs (see, e.g., Roberts et al., "A Structure for Amplified **DNA**", Cell, 33, pp. 53-63 (1983); Dolnick et al., "Correlation of Dihydrofolate Reductase Elevation with Gene Amplification in a Homogeneously Staining. . . Chromosomal Region in L5178Y Cells", J. Cell Biol., 83, pp. 394-402 (1979)). Individual units contain variable amounts of flanking cellular **DNA** and/or carrier **DNA**. Consequently, the repealing units within a partiCular tandem **array** are highly heterogeneous in terms of both size and **sequence** content see, e.g., Roberts et al., id.; Schimke, "Gene Amplification in Cultured Animal Cells", Cell, 37, pp. 703-13 (1980)).

63. 4,948,882, Aug. 14, 1990, Single-stranded labelled oligonucleotides, reactive monomers and methods of synthesis; Jerry L. Ruth, 536/25.32; 435/6; 536/24.3, 25.33, 25.34, 26.6, 26.7, 26.8; 935/77, 78 [IMAGE AVAILABLE]

US PAT NO: 4,948,882 [IMAGE AVAILABLE] L8: 63 of 78

SUMMARY:

BSUM(8)

The prior art methods of enzymatic synthesis require double-stranded **DNA** as a template, and produce double-stranded nucleic acids having label incorporated in both strands. Moveover, the resulting nucleic acids are heterogenous, varying both in **sequence**, length, and in position of the modified bases. Enzymatic synthesis cannot produce a single stranded probe of preselected length, preselected **sequence** having unique reporter groups defined by site and number. Furthermore, the scope of modifications obtainable in the **oligonucleotide** product is severely restricted as the enzymes required for modification can only recognize and incorporate a very limited **array** of modified nucleotides in both strands of a double-stranded, nonuniform nucleic acid. As a result proteins, nucleic acids, carbohydrates, fluorophors,. . .

64. 4,912,039, Mar. 27, 1990, Multidrug resistance in mammalian cell lines and isolation of determinant glycoprotein DNA; John R. Riordan, 435/69.1, 91.41, 172.3, 252.33, 320.1; 536/23.5, 23.53; 935/11, 12 [IMAGE AVAILABLE]

US PAT NO: 4,912,039 [IMAGE AVAILABLE] L8: 64 of 78

DETDESC:

DETD(16)

Southern blot analysis of genomic **DNA** from the drug sensitive and series of related multidrug-resistant CH.sup.R CHO cell lines of FIG 2b is shown in FIG 3a. It is clear that **sequences** homologous to pCHP-1 are amplified in the resistant lines compared with the drug-sensitive or revertant lines. Moreover, the amount of. . . approximately 100 to 1,000 kbp in size, thus the P-glycoprotein gene family is believed to be organized in a tandem **array** within such a region. A similar coordinate increase in amplification of P-glycoprotein genes is not observed in the second-step clone. . . Of interest was the appearance of amplified fragments in the more resistant lines which were not represented in the parental **DNA**. Examples of these are fragments 2 and 5 of FIG. 3a. These may represent "novel joint" regions found in tandemly amplified **sequences** as described in Stark, F. R. and Wahl, G. M. Ann. Rev. Biochem. 53, 447-491 (1984).

65. 4,900,659, Feb. 13, 1990, Nucleotide sequence composition and method for detection of Neisseria gonorrhoeae and method for screening for a nucleotide sequence that is specific for a genetically distinct group; Andrew Lo, et al., 435/6, 871; 436/501; 536/23.7; 935/78 [IMAGE AVAILABLE]

US PAT NO: 4,900,659 [IMAGE AVAILABLE] L8: 65 of 78

DETDESC:

DETD(32)

Stocks of bacteriophage should be expanded and **DNA** prepared (as described in part K) so that an adequate supply of **DNA** for each clone can be obtained. The **DNA** is digested with the appropriate enzyme(s) as determined in the previous step and a vector with the corresponding site(s) is. . . One vector that might be useful would be pIBI 76 since it has a "polylinker" which is an artificially constructed **array** of many commonly used restriction sites. The vector is also designed such that after transformation with a ligation mixture of vector and insert **DNA**, clones can be selected for the presence of vector by resistance to ampicillin and also for the presence of an. . . one will be looking for white colonies instead of white plaques. Clones can then be picked, grown up and plasmid **DNA** isolated using standard procedures described by Maniatis. Clones can then be nick-translated with .sup. 32 P label and identification of clones that are specific for Neisseria gonorrhoeae can be performed as described hereinabove in step H. If clones of **DNA** derived from nucleotide **sequences** that are flanking nucleotide **sequences** of Neisseria gonorrhoeae inserts from ATCC 53409, 53410 or 53411 prove to be specific for Neisseria gonorrhoeae, as defined hereinabove, the nucleotide **sequences** directly adjacent to these flanking nucleotide **sequences** can also be cloned and tested for specificity. This can be repeated by picking clones that are farther and farther away from the original inserts until they are no longer specific for Neisseria gonorrhoeae, and all nucleotide **sequences** beyond that point on the genome are mot flanking nucleotide **sequences** and thus, are not within the scope of the subject invention. The **DNA** inserts of each of the clones that are specific for Neisseria gonorrhoeae define the discrete flanking nucleotide **sequences** on each side of ATCC 534409, ATCC 53410 and ATCC 53411 and thus, are within the scope of the subject. . .

66. 4,885,248, Dec. 5, 1989, Transfer vector; Paul G. Ahlquist, 435/252.33, 172.3, 252.3, 320.1; 536/24.1, 24.2; 935/31, 39, 72, 73 [IMAGE AVAILABLE]

US PAT NO: 4,885,248 [IMAGE AVAILABLE] L8: 66 of 78

DETDESC:

DETD(13)

The vectors used in the present invention for the insertion, propagation and manipulation of the BamHI-ClaI **DNA** fragment from the expression vector pCQV2 (FIG. 1) was M13mp9 (Messing, J. and Vieira, J. (1982) Gene 19:269-276). The M13mp9. . . (e.g., f1 or fd). Other filamentous, single stranded phages could equally well be utilized in these experiments (The Single Stranded **DNA** Phages (1978) Denhardt, D. T., Dressler, D. and D. S. Ray, eds. Cold Springs Harbor Laboratory, New York). M13mp9 was derived from another M13 engineered phage, i.e., M13mp7. The cloning of **DNA** into the replicative form (RF) of M13 has been facilitated by a series of improvements which produced the M13mp7 cloning vehicle (Gronenborn, B. and J. Messing (1978) Nature, Lond. 272:375-377; Messing, J. (1979) Recombinant **DNA** Technical Bulletin, NIH Publication No. 79-99, 2, No. 2 43-48; Messing, J., Crea, R. and P. H. Seeburg (1981) Nucleic. . . IPTG and X-gal (Malamy, M. H., Fiandt, M. and Szybalski, W. (1972) Mol. Gen. Genet. 119:207ff). In addition, a small **DNA** fragment synthesized in vitro and containing an **array** of restriction cleavage sites [a multiple cloning site (MCS)] was inserted into the structural region of the .beta.-galactosidase gene fragment. In spite of these insertions the M13mp7 **DNA** is still infective and the modified lac **DNA** is able to encode the synthesis of a functional .beta.-galactosidase .alpha.-peptide (Langley, K. E., Villarejo, M. R., Fowler, A. V., Zamenhof, P. J. and I. Zabin (1975) Proc. Nat. Acad. Sci. U.S.A. 72:1254-1257). This synthesized **DNA** fragment in M13mp7 contains two sites each for the EcoRI, BamHI, SalI, AccI and HincII restriction enzymes arranges symmetrically with. . . viral (+) strand. This depends on the fragment orientation relative to the M13 genome after ligation. The insertion of a **DNA** fragment into one of these restriction sites is readily monitored because the insertion results in a non-functional .alpha.-peptide and the. . . (Messing, J. and B. Bronenborn (1978) In Denhardt, D. T., Dressler, D. and D. S. Ray (eds.) The Single Stranded **DNA** Phages. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, pp. 449-453). M13mp7 has found wide application in the dideoxy nucleotide **sequencing** procedure (Sanger, F., Nicklen, S. and A. R. Coulsen (1977) Proc. Nat. Acad. Sci. U.S.A. 74:5463-5467).

67. 4,879,012, Nov. 7, 1989, Method for reutilization of electrophoresis gel; Hideki Kambara, et al., 204/157.15, 180.1, 182.8, 299R [IMAGE AVAILABLE]

US PAT NO: 4,879,012 [IMAGE AVAILABLE] L8: 67 of 78

DETDESC:

DETD(3)

Four . . . irradiated with a laser beam 9 generated from a generator 3 for exciting fluorophores, and the fluorescence emitted from fluorescence-labeled **DNA** 7 passing through the detection region is led to a photodiode **array** 16 through a filter 13, a focusing lens 14 and an image intensifier 15. The shorter the **DNA**, the faster the **DNA** migrates. Thus, the base number can be determined from the emission time and the base species can be determined from the track identification. Thus, the **sequence** can be determined from the base number and the base species. An argon laser (488 nm) with 10 mW is used as an exciting light source 3 for determining the **sequence**. The migration is carried out usually for 5 to 6 hours and the **sequence** up

to 300-base **DNA** can be determined. Fluorescence-labeled along DNAs remain between the startpoint of migration and the light-irradiated detection region after the end. . .

68. 4,833,332, May 23, 1989, Scanning fluorescent detection system; Charles W. Robertson, Jr., et al., 250/458.1; 204/180.1, 182.8, 299R; 250/461.2; 356/318, 417 [IMAGE AVAILABLE]

US PAT NO: 4,833,332 [IMAGE AVAILABLE] L8: 68 of 78

DETDESC:

DETD(48)

If . . . program proceeds to determine the identity of the peak. The result is the identity of the next base in the **DNA** **sequence**. The program calculates the function W for the current peak as described above, using the **arrays** D1peak(m) and D2peak(m) as input data. Each nucleotide base will have associated with it a pair of peaks which give a characterstic W. Thus, based on the value of W for this peak, the program gives as output the **DNA** base identity A, T, C, G. The peak point index m and the **arrays** D1peak and D2peak are reset to 0, and the program again enters the upper data acquisition loop as shown in. . .

69. 4,771,002, Sep. 13, 1988, Transcription in plants and bacteria; Stanton B. Gelvin, 435/172.3, 252.2, 252.33, 320.1; 536/23.2, 24.1; 935/30, 35, 56, 72 [IMAGE AVAILABLE]

US PAT NO: 4,771,002 [IMAGE AVAILABLE] L8: 69 of 78

SUMMARY:

BSUM(40)

In contrast to the situation in octopine-type tumors, nopaline T-**DNA** is integrated into the host genome in one continuous fragment (M. Lemmers et al. (1980) J. Mol. Biol. 144:353-376, P. Zambryski et al. (1980) Science 209:1385-1391). Direct tandem repeats were observed. T-**DNA** of plants regenerated from teratomas had minor modifications in the border fragments of the inserted **DNA** (Lemmers et al., supra). **Sequence** analysis of the junction between the right and left borders revealed a number of direct repeats and one inverted repeat.. . . single nucleotide (P. Zambryski et al. (1982) J. Mol. Appl. Genet. 1:361-370). Left and right borders in junctions of tandem **arrays** were separated by spacers which could be over 130 bp. The spacers were of unknown origin and contained some T-**DNA** **sequences**. T-**DNA** was found to be integrated into both repeated and low copy number host **sequences**. H. Joos et al. (1983) Cell 32:1057-1067, have shown that virulence is not eliminated after deletion of one of either of the usual nopaline T-**DNA** border **sequences**.

70. 4,761,367, Aug. 2, 1988, Vectors suitable for detection of eukaryotic DNA regulatory sequences; Marshall H. Edgell, et al., 435/6, 69.1, 69.3, 69.6, 172.3, 240.2, 320.1; 536/23.1, 24.1; 935/9, 27, 32, 70, 71, 77 [IMAGE AVAILABLE]

US PAT NO: 4,761,367 [IMAGE AVAILABLE] L8: 70 of 78

DETDESC:

DETD(44)

Ligations (1 .mu.l or 5 .mu.l) were transformed into E. coli LE392 as described above, and transformants picked into ordered **arrays** on

fresh plates. These colonies were grown overnight and lifted onto nitrocellulose. The filters were hybridized with .sup.32 P-labelled T antigen **DNA** **sequences** as described above. Several positive colonies were identified. Plasmid minipreps were made from these, and diagnostic restriction digests done on. . .

71. 4,719,177, Jan. 12, 1988, Production of complementary DNA representing RNA viral sequences by recombinant DNA methods and uses therefor; David Baltimore, et al., 435/91.51, 172.3, 235.1, 236, 239, 252.3, 252.31, 252.33, 320.1, 849; 536/23.1, 23.72, 24.1; 930/220; 935/12, 18, 19, 21, 22, 56, 65, 73 [IMAGE AVAILABLE]

US PAT NO: 4,719,177 [IMAGE AVAILABLE] L8: 71 of 78

DETDESC:

DETD(56)

Bacterial colonies on tetracycline plates were transferred by toothpick to an **array** on one L-agar plate containing 50 .mu.g/ml ampicillin, and another tetracycline-containing agar plate. Colonies which were identified as ampicillin-sensitive, tetracycline resistant were removed by toothpick to an **array** on a new tetracycline plate, and allowed to grow 18 hours at 37.degree. . These colonies were then screened for poliovirus **DNA** using the colony hybridization technique of Grunstein and Hogness, (1975), PNAS 72:3961-5. Briefly, colonies were transferred to nitrocellulose filters, the bacteria were lysed on the filter and the bacterial **DNA** was fixed onto the nitrocellulose. The filters were then hybridized to an isotopically labeled poliovirus cDNA probe, washed, and autoradiographed. Colonies which retained the radioactive probes were identified as containing poliovirus cDNA **sequences**.

72. 4,666,837, May 19, 1987, DNA sequences, recombinant DNA molecules and processes for producing the A and B subunits of cholera toxin and preparations containing so-obtained subunit or subunits; Nigel Harford, et al., 435/69.3, 69.1, 91.41, 172.3, 243, 252.3, 252.33, 320.1, 849, 909; 436/6, 34, 71; 536/23.1, 23.2, 23.7; 935/11, 12, 29, 72, 73 [IMAGE AVAILABLE]

US PAT NO: 4,666,837 [IMAGE AVAILABLE] L8: 72 of 78

DETDESC:

DETD(43)

The ampicillin resistant transformed colonies obtained in Example 7 are screened for the presence of **DNA** **sequences** hybridizing to the eltB probe by the colony hybridization method described by GERGEN J. et al. Nucl. Acids Res. 7, 2115 (1979). Transformant colonies growing on the solid agar medium are transferred in fixed **arrays** to the surface of duplicate plates of ampicillin containing medium and the plates incubated at 37.degree.. A square of sterile. . .

73. 4,654,419, Mar. 31, 1987, Synthetic polypeptides and antibodies related to epstein-barr virus nuclear antigen; John H. Vaughan, et al., 530/326, 327; 930/10, 224 [IMAGE AVAILABLE]

US PAT NO: 4,654,419 [IMAGE AVAILABLE] L8: 73 of 78

SUMMARY:

BSUM(19)

The correct reading frame of a **DNA** **sequence** coding for a

protein, and therefore the protein's amino acid residue **sequence**, may be determined through the use of antibodies. This strategy involves manufacturing an **array** of protein fragments or polypeptides whose amino acid residue **sequences** correspond to the **sequences** obtained from the three possible gene products. The protein fragments or polypeptides that induce antibodies that immunoreact with the gene's. . .

74. 4,634,665, Jan. 6, 1987, Processes for inserting DNA into eucaryotic cells and for producing proteinaceous materials; Richard Axel, et al., 435/69.1, 69.3, 69.4, 69.5, 69.51, 69.52, 69.6, 172.3, 240.3, 811, 948; 536/23.1, 23.51, 23.52; 935/27, 31, 34, 56, 58, 70 [IMAGE AVAILABLE]

US PAT NO: 4,634,665 [IMAGE AVAILABLE] L8: 74 of 78

DETDESC:

DETD(48)

Cleavage of **DNA** from .PHI.X transformants with Eco RI generates a series of fragments which contain .PHI.X **DNA** **sequences**. These fragments may reflect multiple integration events. Alternatively, these fragments could result from tandem **arrays** of complete or partial .PHI.X **sequences** which are not integrated into cellular **DNA**. To distinguish between these possibilities, transformed cell **DNA** was cut with BAM HI or Eco RI, neither of which cleaves the .PHI.X genome. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. Identical patterns would be generated from undigested **DNA** and from **DNA** cleaved with either of these enzymes. If the **sequences** are integrated, then BAM HI and Eco RI should recognize different sites in the flanking cellular **DNA** and generate unique restriction patterns. **DNA** from clones .PHI.X4 and .PHI.X5 was cleaved with BAM III or Eco RI and analyzed by Southern hybridization. In each. . . pattern with Eco RI fragments differed from that observed with the BAM HI fragments. Furthermore, the profile obtained with undigested **DNA** reveals annealing only in very high molecular weight regions with no discrete fragments observed. Similar observations were made on clone .PHI.X1. Thus, the most of the .PHI.X **sequences** in these three clones are integrated into cellular **DNA**.

75. 4,582,800, Apr. 15, 1986, Novel vectors and method for controlling interferon expression; Robert M. Crowl, 435/69.51, 172.3, 252.3, 252.33, 320.1, 811, 849; 930/142; 935/29, 41, 45, 60 [IMAGE AVAILABLE]

US PAT NO: 4,582,800 [IMAGE AVAILABLE] L8: 75 of 78

DETDESC:

DETD(40)

The term "**DNA** **sequence**" is defined as a linear **array** of nucleotides connected one to the other by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses. The term "codon" as used herein represents a **DNA** **sequence** of three nucleotides (a triplet) which encodes (or "codes for"), through its template or messenger **RNA** ("nRNA"), an amino acid, a translation start signal or a translation termination signal. For example, the nucleotide triplets TTA, TTG,. . .

DETDESC:

DETD(42)

The above nucleotide **sequence** codes for the protein human immune interferon. The term protein (or polypeptide) as used herein, represents a linear **array** of amino acids connected one to the other by peptide bonds between the .alpha.-amino and carboxy groups of adjacent amino acids. The aforementioned nucleotide **sequence** may also be said to comprise a "gene" or a **DNA** **sequence** which codes through its mRNA for a **sequence** of amino acids characteristic of a specific polypeptide, herein the polypeptide human immune interferon.

76. 4,500,786, Feb. 19, 1985, Large area spark chamber and support, and method of recording and analyzing the information on a radioactive work piece; Roy J. Britten, et al., 250/389, 385.2 [IMAGE AVAILABLE]

US PAT NO: 4,500,786 [IMAGE AVAILABLE] L8: 76 of 78

SUMMARY:

BSUM(2)

Many of the most fundamental recombinant **DNA** operations involve gene isolation from recombinant **DNA** libraries, using radioactively labelled probes. The current procedures derive originally from the autoradiographic plaque screening methods of Benton, W. C. and Davis, R. W. (1977), Science 196, 180-182, as applied to recombinant **DNA** genome libraries (e.g., Maniatis, T., Hardison, R. C., Lacy, E., Lauer, J., O'Connell, C., Quon, D., Sim, G. K. and. . . (1978), Cell 15, 687-701). As conventionally carried out sufficient plaques bearing individual recombinant phage are screened so that any given **sequence** will probably occur several times. For the human genome (3,000,000 kb genome size) an average of three occurrences requires about. . . to duplicate 155 mm diameter filters. The phage DNAs are then released by alkali and bound to the filters. The **DNA** matrix on the filter provides more or less faithful reproduction of the random **array** of plaques. After appropriate treatment the filters are hybridized with a radioactive probe, washed thoroughly, dried and autoradiographed under X-ray. . .

77. 4,489,133, Dec. 18, 1984, Two-dimensional crystallization technique; Roger D. Kornberg, 428/408; 378/73; 427/2.13; 428/420, 478.2; 435/7.1, 7.5; 436/547; 530/344, 387.1, 396, 404, 408, 412, 414, 415, 422, 423, 424, 427 [IMAGE AVAILABLE]

US PAT NO: 4,489,133 [IMAGE AVAILABLE] L8: 77 of 78

DETDESC:

DETD(12)

Another category of compounds of interest are **polynucleotides** or nucleic acids, which may include **DNA** or **RNA**, where the **DNA** may be chromosomal, extrachromosomal, plastid e.g. chloroplast or mitochondrial, viral, etc., or **RNA**, such as messenger **RNA**, transfer **RNA**, ribosomal, synthetic, etc. By employing an **oligonucleotide** as a ligand bound to the lipid, one can bind to nucleic acid **sequences** having a complementary **sequence**. These will then be oriented in two-dimensions to form an ordered **array** of nucleotide **sequences** of the same composition.

78. 4,399,216, Aug. 16, 1983, Processes for inserting DNA into eucaryotic cells and for producing proteinaceous materials; Richard Axel, et al., 435/6, 29, 34, 69.1, 69.3, 69.4, 69.51, 69.6, 172.3, 240.26, 320.1, 811, 948; 536/23.1; 935/11, 12, 14, 15, 23, 60, 70, 84 [IMAGE AVAILABLE]

US PAT NO: 4,399,216 [IMAGE AVAILABLE] L8: 78 of 78

DETDESC:

DETD(46)

Cleavage of **DNA** from .PHI.X transformants with Eco RI generates a series of fragments which contain .PHI.X **DNA** **sequences**. These fragments may reflect multiple integration events. Alternatively, these fragments could result from tandem **arrays** of complete or partial .PHI.X **sequences** which are not integrated into cellular **DNA**. To distinguish between these possibilities, transformed cell **DNA** was cut with BAM HI or Eco RI, neither of which cleaves the .PHI.X genome. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. If the .PHI.X **DNA** **sequences** were not integrated, neither of these enzymes would cleave the .PHI.X fragments. Identical patterns would be generated from undigested **DNA** and from **DNA** cleaved with either of these enzymes. If the **sequences** are integrated, then BAM HI and Eco RI should recognize different sites in the flanking cellular **DNA** and generate unique restriction patterns. **DNA** from clones .PHI.X4 and .PHI.X5 was cleaved with BAM III or Eco RI and analyzed by Southern hybridization. In each. . . pattern with Eco RI fragments differed from that observed with the BAM HI fragments. Furthermore, the profile obtained with undigested **DNA** reveals annealing only in very high molecular weight regions with no discrete fragments observed. Similar observations were made on clone .PHI.X1. Thus, the most of the .PHI.X **sequences** in these three clones are integrated into cellular **DNA**.

=>

SEARCH 102 Case #08/327,522

=> d his

(FILE 'HOME' ENTERED AT 14:55:34 ON 31 JUL 95)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:55:39 ON 31 JUL 95
FILE 'MEDLINE'
L1 12137 S ARRAY# OR CHIP# OR BIOCHIP#
FILE 'BIOSIS'
L2 15138 S ARRAY# OR CHIP# OR BIOCHIP#
FILE 'CAPLUS'
L3 54635 S ARRAY# OR CHIP# OR BIOCHIP#
TOTAL FOR ALL FILES
L4 81910 S ARRAY# OR CHIP# OR BIOCHIP#
FILE 'MEDLINE'
L5 368910 S OLIGO# OR OLIGONUCLEOTIDE# OR DNA# OR POLYNUCLEOTIDE#
FILE 'BIOSIS'
L6 395939 S OLIGO# OR OLIGONUCLEOTIDE# OR DNA# OR POLYNUCLEOTIDE#
FILE 'CAPLUS'
L7 319509 S OLIGO# OR OLIGONUCLEOTIDE# OR DNA# OR POLYNUCLEOTIDE#
TOTAL FOR ALL FILES
L8 1084358 S OLIGO# OR OLIGONUCLEOTIDE# OR DNA# OR POLYNUCLEOTIDE#
FILE 'MEDLINE'
L9 303973 S SEQUENC?
FILE 'BIOSIS'
L10 255836 S SEQUENC?
FILE 'CAPLUS'
L11 304896 S SEQUENC?
TOTAL FOR ALL FILES
L12 864705 S SEQUENC?
FILE 'MEDLINE'
L13 1205 S L4 (P) L8
FILE 'BIOSIS'
FILE 'MEDLINE'
L14 1154 S L4 AND L8 AND L12
FILE 'BIOSIS'
L15 868 S L4 AND L8 AND L12
FILE 'CAPLUS'
L16 985 S L4 AND L8 AND L12
TOTAL FOR ALL FILES
L17 3007 S L4 AND L8 AND L12
FILE 'MEDLINE'
L18 627013 S NUCLEASE# OR ENZYM?
FILE 'BIOSIS'
L19 492108 S NUCLEASE# OR ENZYM?
FILE 'CAPLUS'
L20 578432 S NUCLEASE# OR ENZYM?
TOTAL FOR ALL FILES
L21 1697553 S NUCLEASE# OR ENZYM?
FILE 'MEDLINE'
L22 293 S L17 AND L21
FILE 'BIOSIS'
L23 149 S L17 AND L21
FILE 'CAPLUS'
L24 144 S L17 AND L21
TOTAL FOR ALL FILES
L25 586 S L17 AND L21
FILE 'MEDLINE'
L26 285 S L25 NOT PY>1994
FILE 'BIOSIS'
L27 144 S L25 NOT PY>1994

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     FILE 'CAPLUS'
L28          138 S L25 NOT PY>1994
     TOTAL FOR ALL FILES
L29          567 S L25 NOT PY>1994
L30          343 DUPLICATE REMOVE L29 (224 DUPLICATES REMOVED)

=>  d 1,2,8,12,14,26,34,38,39,43,48,58,63,105,107,115,128,141,179,212,215,234
bib ab


L30  ANSWER 1 OF 343  CAPLUS  COPYRIGHT 1995 ACS
AN   1994:458001  CAPLUS
DN   121:58001
TI   Specification method and apparatus for peptide synthesis and
     screening
IN   Hudson, Derek; Johnson, Charles R.; Giebel, Lutz
PA   Arris Pharmaceutical Corp., USA
SO   PCT Int. Appl., 49 pp.
     CODEN: PIXXD2
PI   WO 9405394 A1  940317
DS   W:  AU, CA, JP, NO
     RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AI   WO 93-US8267  930902
PRAI US 92-939065  920902
     US 93-79741  930618
DT   Patent
LA   English
AB   An app. is described for synthesizing a combinatorial library of
     families of biopolymers, such as polypeptides,
     ***oligonucleotides***  and oligosaccharides, on a reusable,
     spatially addressable solid phase plate, typically in  ***arrays***
     of 4 .times. 4 to 400 .times. 400.  In the case of peptides, such as
     synthesis of hexapeptides, the library contains one to three,
     typically two, positions in the  ***sequence***  which are
     uniquely identified by the spatial address location.  The preferred
     plate comprises a hydrophilic polar multi-functionalized polymer
     film coating disks or "winks" of porous polyolefin which are
     removably received in holes in the plate.  The plate is employed
     with a vacuum block system to assist in washing, deprotection of
     protected monomers, such as FMOC-protected amino acids, and
     screening of immobilized, synthesized hexapeptides, for example, to
     det. which synthetic hexapeptides specifically bind to functional
     target proteins, such as  ***enzymes***  , receptors and
     antibodies.  Following identification of the known synthetic
     polypeptides giving the greatest affinity for the arrayed positions
     in the  ***sequence***  , optimal binding for the complete peptide
     ***sequence***  is detd. by an iterative process replacing formerly
     mixed positions with known amino acids at defined spatial addresses.

L30  ANSWER 2 OF 343  CAPLUS  COPYRIGHT 1995 ACS
AN   1995:441211  CAPLUS
DN   122:180275
TI   Method for fractionation of subfragments of a  ***DNA***  sample
     and identification of terminal  ***sequences***
IN   Kambara, Hideki; Okano, Kazunori; Takahashi, Satoshi; Nagai,
     Keiichi; Kawamoto, Hiroko; Furuyama, Hiroko
PA   Hitachi, Ltd., Japan
SO   Eur. Pat. Appl., 17 pp.
     CODEN: EPXXDW
PI   EP 630972 A2  941228
DS   R:  DE, GB
AI   EP 94-109745  940623
PRAI JP 93-155534  930625
     JP 93-189624  930730
```

DT Patent
LA English
AB A ***DNA*** anal. method which comprises attachment of an oligomer of known base ***sequence*** to ***DNA*** fragments obtained by digestion of sample with restriction ***enzymes*** , hybridization between probe oligomers bound to an ***array*** having a random ***sequence*** of several bases following the known ***sequence*** , detn. of presence or absence of the hybridization, identification of the ***DNA*** fragment terminal ***sequence*** from this result, and fractionation of the ***DNA*** fragments and anal. of them is presented. This ***DNA*** anal. method provides for effective anal. of mixts. of long ***DNAs*** or ***DNA*** fragments. The method does not require culturing of recombinant cells and can be automated. Anal. by this method is .apprx.100 times faster than by conventional techniques.

L30 ANSWER 8 OF 343 MEDLINE
AN 94179842 MEDLINE
TI Nucleotide ***sequence*** analysis of natural and combinatorial anti-PDC-E2 antibodies in patients with primary biliary cirrhosis. Recapitulating immune selection with molecular biology.
AU Pascual V; Cha S; Gershwin M E; Capra J D; Leung P S
CS Department of Microbiology, University of Texas Southwestern Medical Center at Dallas 75235.
NC DK 39588 (NIDDK)
IR29 AI 31585-01A1 (NIAID)
A1 12127
+
SO J Immunol, (1994 Mar 1) 152 (5) 2577-85.
Journal code: IFB. ISSN: 0022-1767.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals; Cancer Journals
EM 9406
AB We have analyzed at the nucleotide level the variable region gene ***sequences*** of five human mAbs and five recombinant Fab fragments derived from the mesenteric lymph nodes of patients with primary biliary cirrhosis. Both mAbs and Fabs were monospecific for dihydrolipoamide acetyltransferase, the E2 subunit of the pyruvate dehydrogenase complex, which has been shown to be the major autoantigen of primary biliary cirrhosis. We found that although the mAbs, mainly of the IgM isotype, were encoded by a diverse ***array*** of VH and VL gene segments either as direct copies of germline genes or somatically mutated, the recombinant IgG Fabs expressed clonally related heavy chains displaying a high number of somatic mutations that very likely occurred in the context of Ag selection. Combinatorial pairing of clonally related heavy chains with highly homologous light chains suggests that the IgG anti-pyruvate dehydrogenase complex repertoire of primary biliary cirrhosis patients is the result of the clonal expansion of a restricted set of B cells.

L30 ANSWER 12 OF 343 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 4
AN 95:29367 BIOSIS
DN 98043667
TI Genetic diversity in hard red spring wheat based on ***sequence*** -tagged-site PCR markers.
AU Chen H B; Martin J M; Lavin M; Talbert L E
CS Dep. Plant Soils and Environ. Sci., Montana State Univ., Bozeman, MT 59717-0312, USA
SO Crop Science 34 (6). 1994. 1628-1632. ISSN: 0011-183X
LA English

AB Genetic variation among wheat (Triticum aestivum L.) parents is necessary to derive superior progeny from crossing and selection. However, crosses are often performed among elite lines with similar agronomic and end-use characteristics. Thus, the potential exists for an undesirable narrowing of the germplasm base for any particular class of wheat. The relative genetic diversity within hard red spring wheat was determined in comparison to a sample of wheat accessions representing an ***array*** of types and geographic origins. Three groups of accessions were assayed for the frequencies of ***DNA*** polymorphism using a total of 38 ***sequence*** -tagged-site primer sets with polymerase chain reaction. Group I contained 10 elite hard red spring wheat cultivars under production in Montana and North Dakota, Group II included 15 hard red spring wheat cultivars and lines from the North American Great Plains, and Group III contained 20 accessions representing a wide range of collection and morphological types. Twenty-four of 38 primer sets (63%) and 31 of 76 primer- ***enzyme*** combinations (41%) revealed polymorphisms. The range of genetic similarity estimated by percentage of shared restriction fragments varied from 0.65 to 0.99 among all pairwise comparisons among the 45 lines. Average genetic similarity was 0.81. Genetic similarity among the hard red spring wheats was 0.88, whereas genetic similarity among the broadly based Group HI was 0.78. Our results showed that the breeding pool for hexaploid hard red spring wheat is narrow relative to levels of diversity among and within classes in hexaploid wheat.

L30 ANSWER 14 OF 343 MEDLINE DUPLICATE 5
AN 95187959 MEDLINE
TI In vitro selection of antisense ***oligonucleotides*** targeted to a hairpin structure.
AU Mishra R K; Toulme J J
CS Laboratoire de Biophysique Moleculaire, INSERM U. 386, Universite Bordeaux-II, France.
SO C R Acad Sci III, (1994 Nov) 317 (11) 977-82.
Journal code: CA1. ISSN: 0764-4469.
CY France
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 9506
AB Antisense ***oligonucleotides*** are widely used to selectively prevent pre-RNA splicing, mRNA translation or cDNA synthesis from a retroviral RNA template. However, intramolecular folding of the RNA chain can sequester the target ***sequence*** into a stable structure. Consequently, the antisense effect can be greatly reduced or even abolished. Hydrogen donor and acceptor sites are still available on nucleic acid bases involved in secondary structures. However, the rational design of antisense ***sequences*** able to recognize the three dimensional ***array*** of these sites is not available. We used an in vitro selection procedure to fish out aptastrucs, i.e., oligomers able ("apte") to bind to a structure. A population of randomly synthesized ***oligonucleotides*** was mixed with the structure of interest and oligodeoxynucleotide ***sequences*** bound to the target were selected and amplified. The selection involves the destruction of the unbound candidates by a restriction ***enzyme*** . This procedure can be used both for RNA and ***DNA*** target structures and does not require the purification of the bound ***oligonucleotides*** at each cycle of selection. Several cycles of selection-amplification, followed by cloning and ***sequencing*** , allowed us to identify three ***oligonucleotides*** able to form a complex with a ***DNA*** hairpin. Due to the ***sequence*** of the selected candidates, these aptastruc-hairpin complexes involve very likely non-canonical interactions between the two partners.

L30 ANSWER 26 OF 343 BIOSIS COPYRIGHT 1995 BIOSIS
AN 94:525744 BIOSIS
DN 97538744
TI ***DNA*** ***sequencing*** by hybridization on high density probe ***arrays*** : ***Enzymatic*** enhancement and ***sequence*** reconstruction.
AU Lockhart D J; Chee M S
CS Affymetrix, Santa Clara, CA, USA
SO 44th Annual Meeting of the American Society of Human Genetics, Montreal, Quebec, Canada, October 18-22, 1994. American Journal of Human Genetics 55 (3 SUPPL.). 1994. A264. ISSN: 0002-9297
DT Conference
LA English

L30 ANSWER 34 OF 343 MEDLINE
AN 94166621 MEDLINE
TI Slipped-strand mispairing in a plastid gene: rpoC2 in grasses (Poaceae).
AU Cummings M P; King L M; Kellogg E A
CS Museum of Comparative Zoology, Harvard University.
SO Mol Biol Evol, (1994 Jan) 11 (1) 1-8.
Journal code: MOB. ISSN: 0737-4038.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L25376; GENBANK-L25377; GENBANK-L25378; GENBANK-L25379; GENBANK-L25380; GENBANK-L25381; GENBANK-L25382; GENBANK-L25383; GENBANK-L25384; GENBANK-L25385; GENBANK-L25386
EM 9406
AB An exception to the generally conservative nature of plastid gene evolution is the gene coding for the beta" subunit of RNA polymerase, rpoC2. Previous work by others has shown that maize and rice have an insertion in the coding region of rpoC2, relative to spinach and tobacco. To assess the distribution of this extra coding ***sequence*** , we surveyed a broad phylogenetic sample comprising 55 species from 17 angiosperm families by using Southern hybridization. The extra coding ***sequence*** is restricted to the grasses (Poaceae). ***DNA*** ***sequence*** analysis of 11 species from all five subfamilies within the grass family demonstrates that the extra ***sequence*** in the coding region of rpoC2 is a repetitive ***array*** that exhibits more than a twofold increase in nucleotide substitution, as well as a large number of insertion/deletion events, relative to the adjacent flanking ***sequences*** . The structure of the ***array*** suggests that slipped-strand mispairing causes the repeated motifs and adds to the mechanisms through which the coding ***sequence*** of plastid genes are known to evolve. Phylogenetic analyses based on the ***sequence*** data from grass species support several relationships previously suggested by morphological work, but they are ambiguous about broad relationships within the family.

L30 ANSWER 38 OF 343 MEDLINE
AN 93361502 MEDLINE
TI The rRNA-encoding ***DNA*** ***array*** has an altered structure in topoisomerase I mutants of Saccharomyces cerevisiae.
AU Christman M F; Dietrich F S; Levin N A; Sadoff B U; Fink G R
CS Whitehead Institute for Biomedical Research, 9 Cambridge Center, MA 02142.
NC GM35010 (NIGMS)
SO Proc Natl Acad Sci U S A, (1993 Aug 15) 90 (16) 7637-41.
Journal code: PV3. ISSN: 0027-8424.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 9311
AB All the chromosomes from isogenic TOP1 and top1 strains have similar mobility on pulsed-field gels except for chromosome XII, which fails to migrate into the gels in top1 mutants. Chromosome XII contains the tandem repeats of rRNA-encoding ***DNA*** (rDNA). When a segment of chromosome XII containing only rDNA is transferred to chromosome III by a recombination event, chromosome III fails to enter a pulsed-field gel in extracts from top1 strains, indicating that the aberrant migration of chromosome XII in top1 mutants is caused by the presence of rDNA. Failure of chromosome XII to migrate into a pulsed-field gel occurs only in preparations from exponentially growing top1 cultures and not in preparations from stationary-phase top1 cultures. rDNA from a top1 strain does enter the gel if it is cut with an ***enzyme*** (Pst I) that cuts the tandem rDNA ***array*** into single 9-kb repeat units, indicating that more than a single repeat unit is required to maintain the aberrant structure.

L30 ANSWER 39 OF 343 MEDLINE DUPLICATE 14
AN 94119692 MEDLINE
TI RAPD (arbitrary primer) PCR is more sensitive than multilocus ***enzyme*** electrophoresis for distinguishing related bacterial strains.
AU Wang G; Whittam T S; Berg C M; Berg D E
CS Department of Molecular Microbiology, Washington University Medical School, St Louis, MO 63110.
NC HG00563 (NCHGR)
AI24566 (NIAID)
AI00964 (NIAID)
SO Nucleic Acids Res, (1993 Dec 25) 21 (25) 5930-3.
Journal code: O8L. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 9404
AB The RAPD (random amplified polymorphic ***DNA***) fingerprinting method, which utilizes low stringency PCR amplification with single primers of arbitrary ***sequence*** to generate strain-specific ***arrays*** of anonymous ***DNA*** fragments, was calibrated relative to the widely used, protein-based multilocus ***enzyme*** electrophoretic (MLEE) typing method. RAPD fingerprinting was carried out on five isolates from each of 15 major groups of Escherichia coli strains that cause diarrheal disease worldwide (75 isolates in all). Each group consisted of isolates that were not distinguishable from one another by MLEE typing using 20 diagnostic ***enzyme*** markers. In our RAPD tests, three or more distinct subgroups in each MLEE group were distinguished with each of five primers, and 74 of the 75 isolates were distinguished when data obtained with five primers were combined. Thus, RAPD typing is far more sensitive than MLEE typing for discriminating among related strains of a species. Despite their different sensitivities, the same general relationships among strains were inferred from MLEE and RAPD data. Thus, our results recommend use of the RAPD method for studies of bacterial population genetic structure and evolution, as well as for epidemiology.

L30 ANSWER 43 OF 343 MEDLINE
AN 93233642 MEDLINE
TI (CT)n (GA)n repeats and heat shock elements have distinct roles in chromatin structure and transcriptional activation of the Drosophila

hsp26 gene.
AU Lu Q; Wallrath L L; Granok H; Elgin S C
CS Department of Biology, Washington University, St. Louis, Missouri 63130.
NC GM31532 (NIGMS)
GM07232 (NIGMS)
SO Mol Cell Biol, (1993 May) 13 (5) 2802-14.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 9307
AB Previous analysis of the hsp26 gene of Drosophila melanogaster has shown that in addition to the TATA box and the proximal and distal heat shock elements (HSEs) (centered at -59 and -340, relative to the start site of transcription), a segment of (CT)n repeats at -135 to -85 is required for full heat shock inducibility (R.L. Glaser, G.H. Thomas, E.S. Siegfried, S.C.R. Elgin, and J.T. Lis, J. Mol. Biol. 211:751-761, 1990). This (CT)n element appears to contribute to formation of the wild-type chromatin structure of hsp26, an organized nucleosome ***array*** that leaves the HSEs in nucleosome-free, DNase I-hypersensitive (DH) sites (Q. Lu, L.L. Wallrath, B.D. Allan, R.L. Glaser, J.T. Lis, and S.C.R. Elgin, J. Mol. Biol. 225:985-998, 1992). Inspection of the ***sequences*** upstream of hsp26 has revealed an additional (CT)n element at -347 to -341, adjacent to the distal HSE. We have analyzed the contribution of this distal (CT)n element (-347 to -341), the proximal (CT)n element (-135 to -85), and the two HSEs both to the formation of the chromatin structure and to heat shock inducibility. hsp26 constructs containing site-directed mutations, deletions, substitutions, or rearrangements of these ***sequence*** elements have been fused in frame to the Escherichia coli lacZ gene and reintroduced into the D. melanogaster genome by P-element-mediated germ line transformation. Chromatin structure of the transgenes was analyzed (prior to gene activation) by DNase I or restriction ***enzyme*** treatment of isolated nuclei, and heat-inducible expression was monitored by measuring beta-galactosidase activity. The results indicate that mutations, deletions, or substitutions of either the distal or the proximal (CT)n element affect the chromatin structure and heat-inducible expression of the transgenes. These (CT)n repeats are associated with a nonhistone protein(s) in vivo and are bound by a purified Drosophila protein, the GAGA factor, in vitro. In contrast, the HSEs are required for heat-inducible expression but play only a minor role in establishing the chromatin structure of the transgenes. Previous analysis indicates that prior to heat shock, these HSEs appear to be free of protein. Our results suggest that GAGA factor, an abundant protein factor required for normal expression of many Drosophila genes, and heat shock factor, a specific transcription factor activated upon heat shock, play distinct roles in gene regulation: the GAGA factor establishes and/or maintains the DH sites prior to heat shock induction, while the activated heat shock factor recognizes and binds HSEs located within the DH sites to trigger transcription.

L30 ANSWER 48 OF 343 MEDLINE DUPLICATE 17
AN 93387052 MEDLINE
TI Large ***arrays*** of tandemly repeated ***DNA*** ***sequences*** in the green alga Chlamydomonas reinhardtii.
AU Hails T; Jobling M; Day A
CS Biochemistry Department, Oxford University, UK.
SO Chromosoma, (1993 Jul) 102 (7) 500-7.
Journal code: D7A. ISSN: 0009-5915.

CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 9312
AB We describe the characterization of tandemly repeated ***DNA*** ***sequences*** , which resemble the satellite ***DNA*** ***sequences*** of multicellular eucaryotes, in the unicellular green alga Chlamydomonas reinhardtii. Restriction ***enzymes*** that cleave C. reinhardtii ***DNA*** relatively frequently produce a number of high molecular weight ***DNA*** fragments in addition to the bulk of low molecular weight ***DNA*** fragments. pTANC 1.5 contains a 1.5 kb Sau3A fragment cloned from one of these large bands. pTANC 1.5 hybridized to at least three large ***arrays*** (200 to 700 kb) of tandemly repeated ***DNA*** ***sequences*** in the cell-wall-deficient strain cw1.5. These ***arrays*** are composed of repeat units that are each cleaved once by BamHl into bands of 1.5, 1.9, 2.0 and 2.5 kb in size. The copy numbers of the 1.5, 1.9, 2.0 and 2.5 kb BamHl bands vary between different C. reinhardtii strains. Chlamydomonas smithii and a number of C. reinhardtii strains are deficient in all four BamHl bands. Genetic analysis of wild-type strain 137c, which is deficient in the 2.0 kb BamHl band, indicates that the 1.5, 1.9 and 2.5 kb BamHl bands derive from at least five loci. The 1.5, 1.9 and 2.5 kb repeat units are not extensively interspersed with each other in strain 137c. Pulsed-field gel electrophoresis of intact C. reinhardtii chromosomes indicates that TANC ***arrays*** are present on more than one chromosome.

L30 ANSWER 58 OF 343 MEDLINE DUPLICATE 20
AN 93220833 MEDLINE
TI A simple method of detecting amplified ***DNA*** with immobilized probes on microtiter wells.
AU Kawai S; Maekawajiri S; Yamane A
CS Institute for Biotechnology Research, Wakunaga Pharmaceutical Co., Ltd., Hiroshima, Japan.
SO Anal Biochem, (1993 Feb 15) 209 (1) 63-9.
Journal code: 4NK. ISSN: 0003-2697.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 9307
AB We have developed a simple hybridization method for the detection of specific ***DNA*** ***sequences*** amplified by polymerase chain reaction (PCR). This method is similar to an ***enzyme*** -linked immunosorbent assay (ELISA) format in that labeled PCR products at the 5' termini are hybridized with probes immobilized on a microtiter well and the bound PCR products are detected in a manner similar to that of an ***enzyme*** immunoassay (EIA). Two improvements have been made in immobilizing the probe to the microtiter wells, in terms of increasing both immobility and hybridization efficiency. One is that single-stranded (ss) ***DNA*** , without the complementary strand, is used. The other is that instead of a single copy, a tandem ***array*** of the probe is used for immobilization and hybridization. Using of ssDNA containing about a 60-repeat ***array*** of a relevant ***sequence*** as an immobilized probe, the sensitivity increased 10-fold over that of a single ***oligonucleotide*** unit. We also found that the hybridization conditions such as time, temperature, and solution composition could be simplified. Therefore this method is especially suited for handling of a large number of samples, for example detection of viruses, bacteria, and other pathogens, as well as mot human genetic disorders.

L30 ANSWER 63 OF 343 MEDLINE
AN 94034835 MEDLINE
TI Empirical aspects of strand displacement amplification.
AU Walker G T
CS Becton Dickinson Research Center, Research Triangle Park, North Carolina 27709-2016.
SO PCR Methods Appl, (1993 Aug) 3 (1) 1-6. Ref: 13
Journal code: BNV. ISSN: 1054-9803.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 9402
AB The most attractive feature of SDA is its operation at a single temperature, which removes the need for instrumented temperature cycling as with PCR and the ligase chain reaction. Highly reproducible temperature profiles, over a large ***array*** of samples, can burden the accuracy and expense of an amplification technique. However, the expense of a temperature cycler is offset somewhat by the cost of additional ***enzymes*** used in isothermal techniques. In comparisons with isothermal, transcription-based techniques, SDA requires fewer ***enzymes*** and has a simpler mechanism. SDA may also be more robust than transcription-based processes because it is not susceptible to contaminating ribonuclease activity. This is generally more of a concern when using clinical samples. The most significant disadvantage of SDA is its inability to efficiently amplify long target ***sequences*** . Until this short-coming is eliminated, SDA will be assigned to the diagnostic laboratory along with the ligase chain reaction. Currently, SDA cannot compete with PCR in research applications such as the isolation of gene ***sequences*** . The second disadvantage of SDA is that it operates at relatively low (nonstringent) temperatures, which produces considerable background reactions. Consequently, SDA reaction products cannot be analyzed routinely by ethidium-stained gel electrophoresis, as is used commonly with PCR, unless the target sample contains a large number of initial targets.

L30 ANSWER 105 OF 343 MEDLINE DUPLICATE 34
AN 92052685 MEDLINE
TI A phagemid vector library for cloning ***DNA*** with four-nucleotide 5' or 3' overhangs.
AU Waye M M; Mui F; Hodge K; Li V K
CS Department of Dentistry, University of Toronto, Ontario, Canada.
SO Plasmid, (1991 Jul) 26 (1) 74-7.
Journal code: P8P. ISSN: 0147-619X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X56013; GENBANK-X56014; GENBANK-S70702; GENBANK-S70703; GENBANK-X58180; GENBANK-X56856; GENBANK-X55687; GENBANK-X55688; GENBANK-X55689; GENBANK-X55690
EM 9202
AB A phagemid vector library for cloning ***DNA*** with four nucleotide 5' or 3' overhangs has been constructed. This library is based on the pT7T3 vector (Pharmacia) which is a modification of the phagemid pTZ18U vector. We have chosen pT7T3 as the parent vector because it can be used for Sanger's dideoxy ***sequencing*** and for the generation of RNA probes with either the T7 or T3 promoter. Each member of the cloning vector series pBM has recognition sites

for both of the restriction ***enzymes*** BspM1 and BstX1 in addition to the basic multiple cloning sites. BspM1 recognizes the ***sequence*** 5'...ACCTGC NNNN/NNNN...3' whereas BstX1 recognizes the ***sequence*** 5'...CCAN NNNN/NTGG...3'. Thus these two sites can be overlapped, so that only 256 vectors (instead of 512 vectors) need be constructed to cover all the theoretical possible combinations of sites which give complementary cohesive ends for cloning ***DNA*** with four nucleotide 5' or 3' overhangs. This vector library can be used for amplification cloning of ***DNA*** in a tandem ***array*** by choosing appropriate vectors which have nonpalindromic ***sequences*** . We have obtained approximately 200 members of the 256 possible clones and have organized the vectors using a MacIntosh HyperCard program for easy retrieval.

L30 ANSWER 107 OF 343 MEDLINE
AN 91122493 MEDLINE
TI New techniques for physical mapping of the human genome.
AU Billings P R; Smith C L; Cantor C R
CS Human Genome Center, Lawrence Berkeley Laboratory, Berkeley, California 94720.
SO FASEB J, (1991 Jan) 5 (1) 28-34. Ref: 75
Journal code: FAS. ISSN: 0892-6638.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals; Cancer Journals
EM 9105
AB We describe improvements in techniques and strategies used for making maps of the human genome. The methods currently used are changing and evolving rapidly. Today's techniques can produce ordered ***arrays*** of ***DNA*** fragments and overlapping sets of ***DNA*** clones covering extensive genomic regions, but they are relatively slow and tedious. Methods under development will speed the process considerably. New developments include a range of applications of the polymerase chain reaction, enhanced procedures for high resolution in situ hybridization, and improved methods for generating, manipulating, and cloning large ***DNA*** fragments. More detailed genetic and physical maps will be useful for finding genes, including those associated with human diseases, long before the complete ***DNA*** ***sequence*** of the human genome is available.

L30 ANSWER 115 OF 343 MEDLINE
AN 91056564 MEDLINE
TI Generation of hybrid genes and proteins by vaccinia virus-mediated recombination: application to human immunodeficiency virus type 1 env.
AU Gritz L; Destree A; Cormier N; Day E; Stallard V; Caiazzo T; Mazzara G; Panicali D
CS Applied bioTechnology, Inc, Cambridge, Massachusetts 02142.
NC A126507
SO J Virol, (1990 Dec) 64 (12) 5948-57.
Journal code: KCV. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-M12508; GENBANK-M38707; GENBANK-M38708
EM 9103
AB The ability of poxviruses to undergo intramolecular recombination within tandemly arranged homologous ***sequences*** can be used

to generate chimeric genes and proteins. Genes containing regions of nucleotide homology will recombine to yield a single ***sequence*** composed of portions of both original genes. A recombinant virus containing two genes with a number of conserved regions will yield a population of recombinant viruses containing a spectrum of hybrid ***sequences*** derived by recombination between the original genes. This scheme has been used to generate hybrid human immunodeficiency virus type 1 env genes. Recombinant vaccinia viruses that contain two divergent env genes in tandem ***array*** have been constructed. In the absence of selective pressure to maintain both genes, recombination between conserved homologous regions in these genes generated a wide range of progeny, each of which expressed a novel variant polypeptide encoded by the newly created hybrid env gene. Poxvirus-mediated recombination may be applied to map type-specific epitopes, to create novel pharmaceuticals such as hybrid interferons, to study receptor-binding or ***enzyme*** substrate specificities, or to mimic the antigenic diversity found in numerous pathogens.

L30 ANSWER 128 OF 343 MEDLINE DUPLICATE 46
AN 91055805 MEDLINE
TI Rapid HLA-DPB typing using ***enzymatically*** amplified ***DNA*** and nonradioactive ***sequence*** -specific ***oligonucleotide*** probes [published erratum appears in Immunogenetics 1991;34(6):413].
AU Bugawan T L; Begovich A B; Erlich H A
CS Department of Human Genetics, Cetus Corporation, Emeryville, CA 94608.
SO Immunogenetics, (1990) 32 (4) 231-41.
Journal code: GI4. ISSN: 0093-7711.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-M62326; GENBANK-M62327; GENBANK-M62328; GENBANK-M62329; GENBANK-M62330; GENBANK-M62331; GENBANK-M62332; GENBANK-M62333; GENBANK-M62334; GENBANK-M62335
EM 9103
AB A simple and rapid method for characterizing the polymorphism at the HLA-DPB1 locus has been developed. The procedure involves the selective amplification of the polymorphic second exon of the DPB1 locus by the polymerase chain reaction (PCR), followed by hybridization of the amplified ***DNA*** with 15 nonisotopic ***sequence*** -specific ***oligonucleotide*** probes. There are no ***sequences*** within the second exon of the DPB1 locus that uniquely define an allele; rather, each allele appears to arise from the shuffling of a limited number of polymorphic nucleotide ***sequences*** in six regions of variability. Consequently, individual alleles are identified by the pattern of hybridization of the 15 probes. Two formats for typing are described. In Format I (the dot-blot), the amplified ***DNA*** is ultraviolet (UV) cross-linked to a nylon membrane and hybridized with the ***oligonucleotide*** probes which are covalently labeled with horseradish peroxidase (HRP). In Format II (the reverse dot-blot), the ***oligonucleotides*** , which have poly-T tails, are bound to the membrane and the immobilized ***array*** of probes is hybridized to the PCR product which has incorporated biotinylated primers during the amplification process. In both formats, hybridization is detected by a simple colorimetric reaction. The application of this technology to the fields of tissue typing and individual identity is discussed.

L30 ANSWER 141 OF 343 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 53
AN 89:178018 BIOSIS

DN BA87:89284
TI LINKING NUMBER ANOMALIES IN ***DNA*** UNDER CONDITIONS CLOSE TO CONDENSATION.
AU RINGQUIST S; SHINN R; HANLON S
CS DEP. BIOL. CHEM., UNIV. ILLINOIS COLL. MED., CHICAGO, ILLINOIS 60612.
SO BIOCHEMISTRY 28 (3). 1989. 1076-1085. CODEN: BICHAW ISSN: 0006-2960
LA English
AB Changes in linking numbers and the apparent winding angle of pBR322 ***DNA*** have been evaluated in mixed ethanol-water solvents containing either Na or Mg as the major conunterion contributing to the electrostatic shielding of the duplex. The average number of superhelical turns (.tau.) produced in the standard electrophoresis buffer (Tris-borate-EDTA, pH 8.0) by the transfer of ***DNA*** , relaxed in 200 mM NaCl, 10 mM NaH2PO4/Na2HPO4, and 2 mM EDTA, pH 7, by calf thymus topoisomerase or ligated in 6.6 mM MgCl2, 1 mM KCl, 1 mM ATP, 1 mM dithiothreitol, and 66 mM Tris, pH 7.6, by T4 ligase, was determined as a function of the EtOH concentration. At low ***enzyme*** concentrations, the .tau. values became increasingly more positive in the presence of both cations as the ethanol concentration increased, indicating that the duplex structure was overwound in the ethanol solvents. Winding angle changes between 0 and 20% ethanol, calculated from these values of .tau., exhibited the same correlations with CD spectral properties as had been previously observed for 100% aqueous systems containing monovalent cations [Kilkuskie, R., Wood, N., Shinn, R., Ringquist, S., & Hanlon, S. (1988) Biochemistry 27, 4377-4386]. The results at higher concentrations of ethanol (25-30%), however, were anomalous for the Mg-ligase system. The anomalies increased with higher ethanol, ligase, or Mg concentration. Gel run under these conditions showed enhanced concentrations of slow-moving components, indicative of ligation of intermolecular asssociated ***DNA*** species. At a 10-fold higher level of ligase, ethanol appeared to unwind the duplex, confirming the results of Lee, Mizusawa, and Kakefuda [(1981) Proc. Natl. Acad. Sci. U.S.A. 78, 2838-2842]. All of these anomalies occur under solvent conditions which are close to conditions which produce a heterogeneous dispersion of sedimenting species in ultracentrifugal experiments and compact rodlike structures, visualized by electron microscopy. The circular dichrosim spectra at the onset of the formation of these structures show the characteristics of a chirally packed ***array*** of ***DNA*** duplexes. The reversal of the trend of the ethanol effect on linking number at higher ***enzyme*** and Mg(II) concentrations can be most easily explained by the promotion of the condensation phenomenon by either the ligase or a contaminating factor in the preparation. We suggest that the anomalies in the linking number and winding angle values are due to either ligation of chirally bent ***DNA*** species or a change in the helical period as the linear ***DNA*** adapts to the conformation required for collapse. At ethanol concentrations well below that required for ***DNA*** collapse, the average change in winding angle calculated from the relative lining number appears to be valid and independent of whether the relaxed ***DNA*** species was produced by the topoisomerase or the ligase. In the absence of condensation effects, CD changes are also a reliable index of small average winding angle changes in random- ***sequence*** B-form ***DNA*** in ethanol. Winding angle changes cannot, however, be reliably evaluated by gel methods at or close to conditions where chiral collapse or condensation of ***DNA*** occurs.

L30 ANSWER 179 OF 343 MEDLINE
AN 87311863 MEDLINE
TI Overlapping sets of viral RNAs reflect the ***array*** of polypeptides in the EcoRI J and N fragments (map positions 81.2 to 85.0) of the Autographa californica nuclear polyhedrosis virus

genome.
AU Oellig C; Happ B; Muller T; Doerfler W
SO J Virol, (1987 Oct) 61 (10) 3048-57.
Journal code: KCV. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-M17548
EM 8712
AB In several parts of the Autographa californica nuclear polyhedrosis virus (AcNPV) genome, nested sets of overlapping RNAs with common 3' or 5' termini have been recognized. In the present report, the pattern of viral transcription and the arrangement of viral gene products in the region of 81.2 to 85.0 map units were investigated. In this segment of the AcNPV genome, at least nine size classes of viral RNA were identified which ranged in size from 1.3 kilobases (kb) to 4.6 kb and exhibited common 3' termini. The detailed restriction map and the nucleotide ***sequence*** of this part of the AcNPV genome were determined. Computer analyses revealed several open reading frames (ORFs) on the rightward-transcribed strand with potential TATA and CAAT signals preceding many of the potential ORFs and the 5' termini of some of the mapped RNAs. The leftward-transcribed strand was devoid of major ORFs. The presumptive polypeptides encoded by the larger ORFs ranged in size from 11.3 to 55.6 kilodaltons (kDa). The amino acid ***sequence*** of the presumptive polypeptide encoded by ORF3, a 33.6-kDa molecule, exhibited an unusual, clustered 16-fold repeat of the dipeptide arginine-serine in a protein that showed an overall preponderance of basic amino acids. The results of in vitro translation experiments with hybrid-selected RNAs homologous to internal subfragments of the 81.2- to 85.0-map-unit region yielded polypeptides of approximately 28, 34 to 36, and 48 to 50 kDa, which were close in size to the lengths of the major ORFs derived from the nucleotide ***sequence*** . The localizations of individual size classes of RNAs in the 81.2- to 85.0-map-unit region of the viral genome were determined precisely at the 3' and 5' termini by S1 protection analyses. Within a ***sequence*** of eight nucleotides, all RNAs had the same 3' terminus, which lay close to multiple polyadenylation signals. The initiation sites of the nine different RNA size classes were precisely mapped. As the cap sites of the smaller RNAs (less than 1.8 kb) were determined by S1 protection analyses, a multitude of RNA initiation sites became apparent. It was also shown that the different RNA size classes in the 81.2- to 85.0-map-unit region were detectable as early as 2 h and at least until 36 to 48 h after infection. In unselected cytoplasmic RNA, the size classes of viral RNAs specific for the EcoRI J fragment were detectable early as well as late after infection, although at early times the larger RNAs were detectable in smaller amounts.(ABSTRACT TRUNCATED AT 400 WORDS)

L30 ANSWER 212 OF 343 MEDLINE
AN 86276008 MEDLINE
TI Site-specific ***DNA*** splicing: a general procedure for the creation of a restriction site at a predetermined position in a ***DNA*** ***sequence*** .
AU Kalyan N K; Hung P P; Levner M H; Dheer S K; Lee S G
SO Gene, (1986) 42 (3) 331-7.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 8611

AB A method is described for creating any of a wide ***array*** of restriction sites at a predetermined position in a known ***DNA*** ***sequence*** . The method utilizes the exonuclease activity of BAL 31 and a specially designed bifunctional oligodeoxynucleotide linker. The desired restriction site is generated when the linker is ligated to those BAL 31-digested ***DNA*** fragments which end with the target ***sequence*** . The proper ligation product is then identified by a highly specific hybridization procedure. The method is versatile and specific and is especially useful in the isolation of functional elements of a gene.

L30 ANSWER 215 OF 343 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 82
AN 86:219983 BIOSIS
DN BA81:111283
TI DIGESTION OF THE CHICKEN BETA GLOBIN GENE CHROMATIN WITH MICROCOCCAL ***NUCLEASE*** REVEALS THE PRESENCE OF AN ALTERED NUCLEOSOMAL ***ARRAY*** CHARACTERIZED BY AN ATYPICAL LADDER OF ***DNA*** FRAGMENTS.
AU SUN Y L; XU Y Z; BELLARD M; CHAMBON P
CS SHANGHAI INST. CELL BIOLOGY, ACADEMIA SINICA, 320 YO YANG ROAD, SHANGHAI, CHINA.
SO EMBO (EUR MOL BIOL ORGAN) J 5 (2). 1986. 293-300. CODEN: EMJODG ISSN: 0261-4189
LA English
AB The structure of the chicken adult .beta.-globin gene chromatin in immature and mature erythrocyte nuclei has been analyzed using micrococcal ***nuclease*** digestion. The resulting ***DNA*** fragments were blotted onto DBM-papers and probed with labelled ***DNA*** fragments spanning the adult .beta.-globin gene and its 5'- and 3'-flanking regions. The structure of the nucleosomes within and in the regions flanking the adult .beta.-globin gene appears to be altered in at least two ways in erythrocyte chromatin, when compared with either bulk or inactive ovalbumin gene chromatin. First, oligomeric ***DNA*** fragments containing the .beta.-globin gene are released faster than those of either bulk or ovalbumin gene chromatin. Second, although the difference in size of the liberated oligomeric ***DNA*** fragments is similar to the nucleosomal repeat length of bulk and ovalbumin gene chromatin, the individual oligomers are .apprx. 100 bp shorter than their bulk or ovalbumin gene counterparts, most noticeably when the ***nuclease*** digestion is performed at 37.degree. C. This results in an atypical ladder of .apprx. 300, 500, 700, 900 bp instead of the canonical chicken erythrocyte ladder which is an integral multiple of 207 bp. The same ladder was obtained from immature erythrocytes, in which the .beta.-globin gene is actively transcribed, and from mature erythrocytes, in which it is considered to be inactive with RNA polymerase molecules clustered in the 5' moiety of the gene. This indicates that the alteration of the nucleosomal structure is not due to transcription per se. In addition, several sites hypersensitive to digestion with micrococcal ***nucleases*** are located in both the 5'- and 3'-flanking regions of the .beta.-globin gene in both immature and mature erythrocytes. Our precent results are most easily interpreted by assuming that most of the adult .beta.-globin gene ***sequences*** are organized in an altered nucleosomal ***array*** characterized not only by the absence of the linker-bound H1 and H5 histones, but also by a modification of the nucleosomal cores resulting in a preferential accessibility of .apprx. 40 bp of their ***DNA*** to micrococcal ***nuclease*** digestion. This preferential accessibility may be due to the absence of (H2A-H2B) dimers which are known to be located in the terminal regions of the core ***DNA*** .

L30 ANSWER 234 OF 343 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 88
AN 86:161574 BIOSIS

DN BA81:71990
TI A NEW STRATEGY FOR ORDERED ***DNA*** ***SEQUENCING*** BASED ON A NOVEL METHOD FOR THE RAPID PURIFICATION OF NEAR-MILLIGRAM QUANTITIES OF A CLONED RESTRICTION FRAGMENT.
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SO GENE ANAL TECH 2 (6). 1985 (RECD. 1986). 108-1114. CODEN: GANTDN
ISSN: 0735-0651
LA English
AB A novel method is introduced for generating near-milligram quantities of a specific restriction fragment possessing asymmetric sticky ends in vitro based on hybridizing easily isolated single-stranded ***DNA*** derived from M13 vectors possessing a cloned insert in opposite orientation. The ability to isolate large quantities of a pure, assymmetric restriction fragment allows ***enzymatic*** manipulation of the fragment, resulting in a pure preparation of head-to-head dimers. Bal31 degradation of such dimers can be employed to generate an ordered ***array*** of pure restriction fragments staggered by deletions of about 150 bp from a fixed point. The resulting staggered deletion ***array*** can then be used for forced subcloning into appropriate M13 vectors and directly ***sequenced*** . This ***sequencing*** strategy eliminates the chance of redundant ***sequencing*** by allowing direct, ordered determination of the ***sequence*** of a ***DNA*** fragment from beginning to end.

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